

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2004, 12:21:40 ; Search time 103.591 Seconds
(without alignments)
1241.024 Million cell updates/sec

Title: US-10-021-121-2
Perfect score: 2450
Sequence: 1 MGPPHSGPGGVRVGALLLLG.....TTLLRQRASVEAEAGQHGPL 455

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	8 Query		DB	ID	Description
		Match	Length			
1	2450	100.0	455	2	AAW33698	Aaw33698 AL-2-long
2	1841	75.1	340	2	AAW31544	Aaw31544 Human cyt
3	1841	75.1	340	2	AAW33699	Aaw33699 AL-2-shor
4	1841	75.1	340	2	AAW10637	Aaw10637 NLERK2 li
5	1841	75.1	340	6	ABU07845	Abu07845 Human eph
6	1835	74.9	340	2	AAW17081	Aaw17081 EPH famil
7	1827	74.6	340	2	AAW46615	Aaw46615 Human tra
8	1771	72.3	340	6	ABU07846	Abu07846 Mouse eph
9	628.5	25.7	334	2	AAW00287	Aaw00287 Mouse Eph

10	628.5	25.7	336	2	AAR92742	Aar92742	Murine he
11	626.5	25.6	336	6	ABU07844	Abu07844	Mouse eph
12	623	25.4	346	2	AAR55059	Aar55059	Elk tyros
13	623	25.4	346	2	AAR91930	Aar91930	Human cyt
14	623	25.4	346	2	AAW19249	Aaw19249	Human elk
15	623	25.4	346	2	AAW36055	Aaw36055	Human elk
16	623	25.4	346	2	AAW44323	Aaw44323	Human elk
17	623	25.4	346	6	ABU07841	Abu07841	Human eph
18	623	25.4	346	7	ABU62401	Abu62401	Human elk
19	622	25.4	346	2	AAR82606	Aar82606	Eph trans
20	621.5	25.4	331	2	AAW00288	Aaw00288	Chicken E
21	620.5	25.3	333	2	AAR94655	Aar94655	Ligand fo
22	620.5	25.3	333	2	AAR92743	Aar92743	Human hep
23	620.5	25.3	333	2	AAR89287	Aar89287	Human LER
24	620.5	25.3	333	2	AAW06337	Aaw06337	Full leng
25	620.5	25.3	333	2	AAW11308	Aaw11308	Receptor-
26	620.5	25.3	333	6	ABU07886	Abu07886	Novel hum
27	620.5	25.3	333	7	ADD89059	Add89059	TAT245. 1
28	610.5	24.9	308	2	AAR94656	Aar94656	Ligand fo
29	610.5	24.9	308	2	AAW06334	Aaw06334	Ligand #2
30	604.5	24.7	345	6	ABU07842	Abu07842	Mouse eph
31	483	19.7	89	3	AAAY71438	Aay71438	Human eph
32	458.5	18.7	658	3	AAAY96782	Aay96782	Ephrin-B2
33	456	18.6	254	6	ABU07843	Abu07843	Human eph
34	454	18.5	683	3	AAAY96781	Aay96781	Ephrin-B1
35	447	18.2	229	5	AAE24019	Aae24019	Murine ep
36	443	18.1	229	5	AAE24020	Aae24020	Human eph
37	431.5	17.6	195	2	AAW06333	Aaw06333	Ligand #1
38	431.5	17.6	195	2	AAW11307	Aaw11307	Receptor-
39	284.5	11.6	92	4	AAM37671	Aam37671	Peptide #
40	284.5	11.6	92	5	ABG46524	Abg46524	Human pep
41	196.5	8.0	136	4	AAM37534	Aam37534	Peptide #
42	196.5	8.0	136	5	ABG46394	Abg46394	Human pep
43	195	8.0	82	3	AAAY71437	Aay71437	Human eph
44	193.5	7.9	106	3	AAB54187	Aab54187	Human pan
45	192	7.8	82	3	AAAY71436	Aay71436	Human eph

ALIGNMENTS

RESULT 1

AAW33698

ID AAW33698 standard; protein; 455 AA.

XX

AC AAW33698;

XX

DT 30-APR-1998 (first entry)

XX

DE AL-2-long (AL-21) protein.

XX

KW AL-21; AL-2; AL-2-long; human; treatment; neurological disorder; tumour;
 KW rheumatoid arthritis; wound healing; paralysis; angiogenesis; leukaemia;
 KW psoriasis; Alzheimer's disease; epilepsy.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
FT	Peptide	1. .26
FT		/note= "signal peptide"
FT	Protein	27. .455
FT		/note= "mature protein"
FT	Domain	27. .219
FT		/note= "extracellular domain"
FT	Domain	220. .245
FT		/note= "hydrophobic transmembrane domain"
XX		
PN	WO9740153-A1.	
XX		
PD	30-OCT-1997.	
XX		
PF	17-APR-1997; 97WO-US006345.	
XX		
PR	19-APR-1996; 96US-00635130.	
XX		
PA	(GETH) GENENTECH INC.	
XX		
PI	Caras IW;	
XX		
DR	WPI; 1997-535837/49.	
DR	N-PSDB; AAV06354.	
XX		
PT	Human AL-2 neurotrophic factor and related DNA - used to develop products	
PT	for, e.g. treating neurologic disorders, angiogenesis disorders, tumours	
PT	or rheumatoid arthritis or for wound healing.	
XX		
PS	Claim 20; Fig 1A-C; 86pp; English.	
XX		
CC	This is a AL-2-long (AL-21) protein. The AL-2 is a novel Eph-related	
CC	tyrosine kinase receptor ligand. AL-2 can be administered to patients in	
CC	whom the nervous system has been damaged by trauma, surgery, stroke,	
CC	ischaemia, infection, metabolic disease, nutritional deficiency,	
CC	malignancy, or toxic agents, to promote the survival or growth of	
CC	neurons. They can be used to treat motoneuron disorders such as	
CC	amyotrophic lateral sclerosis (Lou Gehrig's disease), Bell's palsy, and	
CC	various conditions involving spinal muscular atrophy, or paralysis. AL-2	
CC	can be used to treat human neurodegenerative disorders, such as	
CC	Alzheimer's disease, Parkinson's disease, epilepsy, demyelinating	
CC	diseases such as multiple sclerosis, Huntingtons chorea, Down's syndrome,	
CC	nerve deafness, Menier's disease, and other disorders of the cerebellum.	
CC	AL-2 can be used as cognitive enhancer, to enhance learning particularly	
CC	in dementias or trauma, since they can promote axonal outgrowth and	
CC	synaptic plasticity, particularly of hippocampal neurons that express AL-	
CC	2 binding Eph-family receptors and cortical neurons that express AL-2. AL	
CC	-2 can also be used for wound healing, i.e. accelerating	
CC	neovascularisation of, e.g. burns and ulcers. The encoding nucleic acids	
CC	are useful in preparing antibodies that specifically bind to the AL-2	
CC	protein. The antibodies and the AL-2 antagonists are useful in diagnosing	
CC	and treating various neuronal disorders. AL-2 antagonists can be used for	
CC	modulating angiogenesis. They can also be used for the treatment of	
CC	tumours, acute myeloid leukaemia (AML), chronic myeloid leukaemia (CML),	
CC	myelodysplastic syndrome (MDS), diabetic retinopathy, neovascular	
CC	glaucoma, psoriasis and rheumatoid arthritis	
XX		

SQ Sequence 455 AA;

Query Match 100.0%; Score 2450; DB 2; Length 455;
Best Local Similarity 100.0%; Pred. No. 2.1e-197;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY      1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

QY     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLTCDRDLRFTIKFQEY 120
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLTCDRDLRFTIKFQEY 120

QY    121 SPNLWGHEFRSHHDYIIATSDGTREGLESQGVCVCLTRGMKVLLRVGQSPRGGA VPRKP 180
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 SPNLWGHEFRSHHDYIIATSDGTREGLESQGVCVCLTRGMKVLLRVGQSPRGGA VPRKP 180

QY    181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

QY    241 GVAGAGGAMCWRRRRRAKPSERHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGG 300
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GVAGAGGAMCWRRRRRAKPSERHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGG 300

QY    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPNNIYYTSSISVLEWPILHTIQLFFMRSK 360
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPNNIYYTSSISVLEWPILHTIQLFFMRSK 360

QY    361 CSRVTTFLEFPVQVITTSTCRMTSFSFTTLNPSMQACRAQMGEFRIRWCFWGDRILGTALF 420
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 CSRVTTFLEFPVQVITTSTCRMTSFSFTTLNPSMQACRAQMGEFRIRWCFWGDRILGTALF 420

QY    421 VLVLILLLLGRLNMHQTTLLRQRASVEAEAGQHGPL 455
      ||||||||||||||||||||||||||||||||||||||||
Db    421 VLVLILLLLGRLNMHQTTLLRQRASVEAEAGQHGPL 455
```

RESULT 2

AAW31544

ID AAW31544 standard; protein; 340 AA.

XX

AC AAW31544;

XX

DT 14-APR-1998 (first entry)

XX

DE Human cytokine Lerk-8.

XX

KW Lerk-8; cytokine; human; hek; elk; receptor tyrosine kinase; ligand;

KW neurodegenerative disease; wound healing; neovascularisation; diagnosis;

KW therapy.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1. .27

FT /label= Sig_peptide
 FT Protein 28. .340
 FT /label= Mat_protein
 FT Domain 28. .224
 FT /note= "extracellular domain"
 FT Modified-site 210. .212
 FT /note= "N-glycosylated"
 FT Domain 225. .251
 FT /note= "transmembrane domain"
 FT Domain 252. .340
 FT /note= "cytoplasmic domain"
 FT Misc-difference 325
 FT /note= "residue 325 is Leu in Lerk-8 variant"
 XX
 PN WO9736919-A2.
 XX
 PD 09-OCT-1997.
 XX
 PF 19-MAR-1997; 97WO-US004533.
 XX
 PR 21-MAR-1996; 96US-00621146.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Cerretti DP;
 XX
 DR WPI; 1997-503043/46.
 DR N-PSDB; AAT89519.
 XX
 PT New isolated cytokine, Lerk-8 - binds to the hek and elk receptor
 PT tyrosine kinases, used to develop products for diagnosis and therapy.
 XX
 PS Claim 3; Page 32-33; 37pp; English.
 XX
 CC This protein sequence comprises a novel human cytokine designated Lerk-8.
 CC The amino acid sequence was deduced from a human foetal brain cDNA clone
 CC (see AAT89519). Lerk-8 binds to the cell surface receptors hek and elk,
 CC which are members of the eph/elk family of receptor tyrosine kinases.
 CC Lerk-8 polypeptides, especially soluble polypeptides comprising amino
 CC acid residues -27 to 142-197 of the full-length protein, can be expressed
 CC in transformed host cells. These polypeptides can be used to purify hek
 CC or elk proteins, and to purify or identify cells that express hek or elk
 CC on the surface. Such cells can be used in various in vitro studies or in
 CC vivo procedures, e.g. neural cells expressing elk can be administered to
 CC a mammal afflicted with a neurodegenerative disorder. The Lerk-8
 CC polypeptides can also be used to deliver diagnostic or therapeutic agents
 CC to these cells (e.g. leukaemia cells). The Lerk-8 DNA and polypeptides
 CC can also be used to: treat disorders mediated by defective or
 CC insufficient amounts of Lerk-8; to treat disorders such as injury to
 CC neural tissue or neurologic disease; to promote angiogenesis; and for
 CC wound healing or stimulating neovascularisation of grafted tissues
 XX
 SQ Sequence 340 AA;

Query Match 75.1%; Score 1841; DB 2; Length 340;
 Best Local Similarity 100.0%; Pred. No. 2.4e-146;
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRDL	60
Db	1	MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRDL	60
QY	61	LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRDLRFTIKFQEY	120
Db	61	LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRDLRFTIKFQEY	120
QY	121	SPNLWGHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGAVPRKP	180
Db	121	SPNLWGHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGAVPRKP	180
QY	181	VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL	240
Db	181	VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL	240
QY	241	GVAGAGGAMCWRRRRRAKPSESRRHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGG	300
Db	241	GVAGAGGAMCWRRRRRAKPSESRRHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGG	300
QY	301	GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY	338
Db	301	GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY	338

RESULT 3

AAW33699

ID AAW33699 standard; protein; 340 AA.

XX

AC AAW33699;

XX

DT 30-APR-1998 (first entry)

XX

DE AL-2-short (AL-2s) protein.

XX

KW AL-2s; AL-2; AL-2-short; human; treatment; neurological disorder; tumour;
 KW rheumatoid arthritis; wound healing; paralysis; angiogenesis; leukaemia;
 KW psoriasis; Alzheimer's disease; epilepsy.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	Peptide	1. .26
----	---------	--------

FT		/note= "signal peptide"
----	--	-------------------------

FT	Protein	27. .340
----	---------	----------

FT		/note= "mature protein"
----	--	-------------------------

FT	Domain	27. .219
----	--------	----------

FT		/note= "extracellular domain"
----	--	-------------------------------

FT	Domain	220. .245
----	--------	-----------

FT		/note= "hydrophobic transmembrane domain"
----	--	---

XX

PN WO9740153-A1.

XX

PD 30-OCT-1997.

XX

PF 17-APR-1997; 97WO-US006345.

XX
 PR 19-APR-1996; 96US-00635130.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Caras IW;
 XX
 DR WPI; 1997-535837/49.
 DR N-PSDB; AAV06355.
 XX
 PT Human AL-2 neurotrophic factor and related DNA - used to develop products
 PT for, e.g. treating neurologic disorders, angiogenesis disorders, tumours
 PT or rheumatoid arthritis or for wound healing.
 XX
 PS Claim 20; Fig 2A-B; 86pp; English.
 XX
 CC This is a AL-2-short (AL-2s) protein. The AL-2 is a novel Eph-related
 CC tyrosine kinase receptor ligand. AL-2 can be administered to patients in
 CC whom the nervous system has been damaged by trauma, surgery, stroke,
 CC ischaemia, infection, metabolic disease, nutritional deficiency,
 CC malignancy, or toxic agents, to promote the survival or growth of
 CC neurons. They can be used to treat motoneuron disorders such as
 CC amyotrophic lateral sclerosis (Lou Gehrig's disease), Bell's palsy, and
 CC various conditions involving spinal muscular atrophy, or paralysis. AL-2
 CC can be used to treat human neurodegenerative disorders, such as
 CC Alzheimer's disease, Parkinson's disease, epilepsy, demyelinating
 CC diseases such as multiple sclerosis, Huntingtons chorea, Down's syndrome,
 CC nerve deafness, Menier's disease, and other disorders of the cerebellum.
 CC AL-2 can be used as cognitive enhancer, to enhance learning particularly
 CC in dementias or trauma, since they can promote axonal outgrowth and
 CC synaptic plasticity, particularly of hippocampal neurons that express AL-
 CC 2 binding Eph-family receptors and cortical neurons that express AL-2. AL
 CC -2 can also be used for wound healing, i.e. accelerating
 CC neovascularisation of, e.g. burns and ulcers. The encoding nucleic acids
 CC are useful in preparing antibodies that specifically bind to the AL-2
 CC protein. The antibodies and the AL-2 antagonists are useful in diagnosing
 CC and treating various neuronal disorders. AL-2 antagonists can be used for
 CC modulating angiogenesis. They can also be used for the treatment of
 CC tumours, acute myeloid leukaemia (AML), chronic myeloid leukaemia (CML),
 CC myelodysplastic syndrome (MDS), diabetic retinopathy, neovascular
 CC glaucoma, psoriasis and rheumatoid arthritis
 XX
 SQ Sequence 340 AA;

Query Match 75.1%; Score 1841; DB 2; Length 340;

Best Local Similarity 100.0%; Pred. No. 2.4e-146;

Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGPPHSGPGGVRVGALLLLGLVGLVSGLSLEPVYWN	SANKRFQAEGGYVLYPQIGDRLDL	60
Db	1	MGPPHSGPGGVRVGALLLLGLVGLVSGLSLEPVYWN	SANKRFQAEGGYVLYPQIGDRLDL	60
Qy	61	LCPRARPPGPHSSPNYEFYKLYLVGGAQGR	RCEAPPAPNLLLTCDRPDLDLRFTIKFQEY	120
Db	61	LCPRARPPGPHSSPNYEFYKLYLVGGAQGR	RCEAPPAPNLLLTCDRPDLDLRFTIKFQEY	120
Qy	121	SPNLWGHEFRSHHDYIIATSDGTREGLES	LQGGVCLTRGMKVLLRVGQSPRGGA	180

```

      |||
Db      121 SPNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
Qy      181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
      |||
Db      181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
Qy      241 GVAGAGGAMCWRRRRRAKPSES RHPGPSFGRGGS LGLGGGGMGPREAEPGELGIALRGG 300
      |||
Db      241 GVAGAGGAMCWRRRRRAKPSES RHPGPSFGRGGS LGLGGGGMGPREAEPGELGIALRGG 300
Qy      301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
      |||
Db      301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338

```

RESULT 4

AAW10637

ID AAW10637 standard; protein; 340 AA.

XX

AC AAW10637;

XX

DT 23-JUN-1997 (first entry)

XX

DE NLERK2 ligand for eph-related kinase.

XX

KW LERK; ligand for eph-related kinase; ERK; NLERK2;

KW receptor protein tyrosine kinase; cell proliferation;

KW cell differentiation; cell survival; nerve cell.

XX

OS Homo sapiens.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	Peptide	1. .29
----	---------	--------

FT		/label= Sig_peptide
----	--	---------------------

FT	Protein	30. .340
----	---------	----------

FT		/label= Mat_protein
----	--	---------------------

FT	Modified-site	210
----	---------------	-----

FT		/label= N-glycosylation_site
----	--	------------------------------

FT	Domain	227. .251
----	--------	-----------

FT		/label= Transmembrane_domain
----	--	------------------------------

XX

PN WO9704091-A1.

XX

PD 06-FEB-1997.

XX

PF 19-JUL-1996; 96WO-AU000460.

XX

PR 20-JUL-1995; 95AU-00004263.

PR 27-NOV-1995; 95AU-00006847.

PR 22-DEC-1995; 95AU-00007299.

PR 05-FEB-1996; 96AU-00007890.

XX

PA (AMRA-) AMRAD OPERATIONS PTY LTD.

XX

PI Nicola NA;

XX

DR WPI; 1997-132632/12.
 DR N-PSDB; AAT60966.
 XX
 PT Nucleic acid mol. encoding ligand for eph-related kinase - useful for
 PT treatment of, pref. neuronal, cells to increase survival, proliferation
 PT and differentiation.
 XX
 PS Claim 16; Page 37-39; 71pp; English.
 XX
 CC A novel human ligand for eph-related kinase (LERK) is designated NLERK2
 CC (AAW10637). It is encoded by a cDNA clone (AAT60966) obtd. from a human
 CC foetal brain cDNA library. The novel receptor ligand can be expressed in
 CC transformed host cells and used in methods for regulating the
 CC development, maintenance or regeneration of different cells (e.g.
 CC neurons) and tissues in vivo and in vitro. Soluble NLERK2 peptides can be
 CC used to treat injury, disease or abnormality in the nervous system, and
 CC membrane-bound NLERK2 to modulate proliferation, different or survival
 CC e.g. in grafting procedures or transplantation. NLERK2 can also be used
 CC to raise antibodies for use in immunotherapy, and to detect anti-NLERK2
 CC antibodies that may occur in some autoimmune diseases
 XX
 SQ Sequence 340 AA;

Query Match 75.1%; Score 1841; DB 2; Length 340;
 Best Local Similarity 100.0%; Pred. No. 2.4e-146;
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy      1 MGPPHSGPGGVRVGALLLLGLVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
          |||
Db      1 MGPPHSGPGGVRVGALLLLGLVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRDLRFTIKFQEY 120
          |||
Db     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRDLRFTIKFQEY 120

Qy    121 SPNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
          |||
Db    121 SPNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy    181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
          |||
Db    181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy    241 GVAGAGGAMCWRRRRRAKPSERHPGPGSFGRGGS LGLGGGGMGMPREAEPEGELGIALRGG 300
          |||
Db    241 GVAGAGGAMCWRRRRRAKPSERHPGPGSFGRGGS LGLGGGGMGMPREAEPEGELGIALRGG 300

Qy    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPNNIYY 338
          |||
Db    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPNNIYY 338

```

RESULT 5
 ABU07845
 ID ABU07845 standard; protein; 340 AA.
 XX
 AC ABU07845;

XX
 DT 10-MAY-2003 (first entry)
 XX
 DE Human ephrin-B3 ligand.
 XX
 KW Cytostatic; vasodilator; antiinflammatory; cardiant; gene therapy;
 KW ligand-receptor binding modulator; ephrin ligand; angiogenesis;
 KW lymphangiogenesis; aberrant Ephrin-Tie biology; cell growth disorder;
 KW cell migration disorder; cell proliferation disorder; neovascularisation;
 KW ischaemia; infarction; tissue graft; transplant; human; ephrin-B3;
 KW tie receptor tyrosine kinase; Eph receptor ligand.
 XX
 OS Homo sapiens.
 XX
 PN WO2003004529-A2.
 XX
 PD 16-JAN-2003.
 XX
 PF 02-JUL-2002; 2002WO-IB002524.
 XX
 PR 02-JUL-2001; 2001US-0302960P.
 XX
 PA (LICN) LICENTIA LTD.
 XX
 PI Alitalo K, Kubo H;
 XX
 DR WPI; 2003-210341/20.
 DR N-PSDB; ABX12546.
 XX
 PT Identifying modulators of binding between a Tie receptor tyrosine kinase
 PT and an Ephrin ligand, useful for promoting neovascularization, comprises
 PT contacting a Tie receptor with an Ephrin in the presence of a putative
 PT modulator.
 XX
 PS Disclosure; Page 117-119; 199pp; English.
 XX
 CC The invention describes a method of identifying a modulator of binding
 CC between a Tie receptor tyrosine kinase and an Ephrin ligand. The method
 CC comprises contacting a Tie receptor composition with an Ephrin
 CC composition in the presence and in the absence of a putative modulator
 CC compound, and detecting the binding between Tie receptor and the Ephrin
 CC in the presence and in the absence of the putative modulator. The method
 CC is useful for identifying a modulator of binding between a Tie receptor
 CC tyrosine kinase and an Ephrin ligand. Modulators identified from the
 CC method are useful in modulating angiogenic processes, including
 CC lymphangiogenesis, for treating diseases associated with aberrant Ephrin-
 CC Tie biology, aberrant growth, migration or proliferation of cells that
 CC express a Tie receptor, or for promoting growth of vessel or
 CC neovascularisation (e.g. ischaemic tissue, an infarction, a new or
 CC chronic compound, or a tissue graft or transplant). This is the amino
 CC acid sequence of human Ephrin-B3, a member of the Ephrin-B subclass of
 CC ligands that are bound to the membrane via a transmembrane domain and
 CC short cytoplasmic tail and function as Eph receptor ligands
 XX
 SQ Sequence 340 AA;

Query Match

75.1%; Score 1841; DB 6; Length 340;

Best Local Similarity 100.0%; Pred. No. 2.4e-146;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEAGGYVLYPQIGDRLDL 60
        |||
Db      1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEAGGYVLYPQIGDRLDL 60

Qy     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
        |||
Db     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy    121 SPNLWGHEFRSHHDYIIATSDGTREGLESIQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
        |||
Db    121 SPNLWGHEFRSHHDYIIATSDGTREGLESIQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy    181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
        |||
Db    181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy    241 GVAGAGGAMCWRRRRRAKPSERHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGG 300
        |||
Db    241 GVAGAGGAMCWRRRRRAKPSERHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGG 300

Qy    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
        |||
Db    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
```

RESULT 6

AAW17081

ID AAW17081 standard; protein; 340 AA.

XX

AC AAW17081;

XX

DT 09-AUG-1997 (first entry)

XX

DE EPH family ligand Efl-6.

XX

KW Efl-6; Eph; Elk; receptor tyrosine kinase; signal transduction; ligand;
KW neurological disease.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1. .24

FT /label= Sig_peptide

FT Protein 25. .340

FT /label= Mat_protein

FT Misc-difference 166

FT /label= Gln, Arg

FT Domain 225. .249

FT /label= Transmembrane_domain

XX

PN W09715667-A1.

XX

PD 01-MAY-1997.

XX

PF 25-OCT-1996; 96WO-US017201.
 XX
 PR 25-OCT-1995; 95US-0007015P.
 XX
 PA (REGE-) REGENERON PHARM INC.
 XX
 PI Davis S, Gale NW, Yancopoulos GD;
 XX
 DR WPI; 1997-259021/23.
 DR N-PSDB; AAT69808.
 XX
 PT New nucleic acid encoding Efl-6 ligand protein - used for promoting
 PT growth and proliferation of neuronal cells and in drug screening.
 XX
 PS Claim 2; Fig 1; 36pp; English.
 XX
 CC A novel ligand (AAW17081), designated Efl-6 (or Eph transmembrane
 CC tyrosine kinase family ligand 6), binds to the Elk, Nuk/Cek5, Hek2/Sek4,
 CC Htk and Sek1 receptors on cells. Its amino acid sequence was deduced from
 CC a human frontal cortex cDNA clone (AAT69808). Recombinant Elf-6,
 CC truncated soluble polypeptides comprising the extracellular domain of Elf
 CC -6, and Efl-6 ligandbodies comprising soluble Efl-6 and the Fc portion of
 CC IgG can be expressed in host cells. These can be used to support neuronal
 CC and other Eph receptor-bearing cell populations for treatment of
 CC neurological disorders, in drug screening and to raise diagnostic
 CC antibodies
 XX
 SQ Sequence 340 AA;

Query Match 74.9%; Score 1835; DB 2; Length 340;
 Best Local Similarity 99.7%; Pred. No. 7.8e-146;
 Matches 337; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	MGPPHSGPGGVRVGALLLLGLVGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL	60
Db	1	MGPPHSGPGGVRVGALLLLGLVGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL	60
Qy	61	LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRPDLDLRFTIKFQEY	120
Db	61	LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRPDLDLRFTIKFQEY	120
Qy	121	SPNLWGHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGAVPRKP	180
Db	121	SPNLWGHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLXVGQSPRGGAVPRKP	180
Qy	181	VSEMPMERDRGAAHSLEPGKENLPGDPTSNAATSRGAEGPLPPPSMPAVAGAAGGLALLLL	240
Db	181	VSEMPMERDRGAAHSLEPGKENLPGDPTSNAATSRGAEGPLPPPSMPAVAGAAGGLALLLL	240
Qy	241	GVAGAGGAMCWRRRRAKPSERHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGG	300
Db	241	GVAGAGGAMCWRRRRAKPSERHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGG	300
Qy	301	GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY	338
Db	301	GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY	338

RESULT 7

AAW46615

ID AAW46615 standard; protein; 340 AA.

XX

AC AAW46615;

XX

DT 06-JUL-1998 (first entry)

XX

DE Human transmembrane ligand Elk-L3.

XX

KW Elk-L3; Elk-related receptor tyrosine kinase; transmembrane ligand;

KW human; signal transduction; axonogenesis; nerve cell; neurone;

KW Alzheimer's disease; Parkinson's disease; Huntingdon's disease;

KW demyelination; multiple sclerosis; amyotrophic lateral sclerosis;

KW nervous system infection; Wernicke's disease; trauma; ischaemia; stroke;

KW nutritional polyneuropathy; progressive supranuclear palsy;

KW Shy Drager's syndrome; multistem degeneration;

KW olivo ponto cerebellar atrophy, peripheral nerve damage.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 166

FT /label= Gln, Arg

FT Domain 225..249

FT /note= "transmembrane domain"

XX

PN WO9801548-A1.

XX

PD 15-JAN-1998.

XX

PF 04-JUL-1997; 97WO-CA000473.

XX

PR 05-JUL-1996; 96US-0021272P.

XX

PA (MOUN) MOUNT SINAI HOSPITAL CORP.

XX

PI Holland S, Mbamalu G, Pawson T;

XX

DR WPI; 1998-101047/09.

DR N-PSDB; AAV16097.

XX

PT Modulating transmembrane ligand for an Elk-related receptor tyrosine

PT kinase - by formation of a complex between an oligomerised Elk-related

PT receptor tyrosine kinase and a transmembrane ligand.

XX

PS Disclosure; Fig 5A; 40pp; English.

XX

CC This polypeptide comprises human Elk-L3, a transmembrane ligand of Elk-

CC related receptor tyrosine kinase (ERRTK). A novel method of modulating

CC the biological activity of, or for affecting a pathway regulated by, a

CC transmembrane ligand for an ERRTK in a cell expressing the transmembrane

CC ligand comprises forming a complex between a purified and isolated

CC oligomerised ERRTK, or an isoform or an extracellular domain of the

CC ERRTK, and the transmembrane ligand expressed on the cell. The complex

CC can also be used for evaluating a substance for its ability to modulate

CC the biological activity of a transmembrane ligand for an ERRTK, and to
 CC identify substances that affect or modulate a pathway regulated by a
 CC ERRTK. A purified and isolated oligomerised ERRTK can be used in the
 CC preparation of a medicament for modulating neuronal development or
 CC regeneration in a subject, or in a medicament for modulating axonogenesis
 CC in a subject (all claimed). The substances identified by the methods can
 CC be used to modulate axonogenesis, nerve cell interactions and
 CC regeneration, to treat diseases and conditions involving trauma and
 CC injury to the nervous system, such as Alzheimer's disease, Parkinson's
 CC disease, Huntingdon's disease, demyelinating diseases, such as multiple
 CC sclerosis, amyotrophic lateral sclerosis, bacterial and viral infections
 CC of the nervous system, deficiency diseases, such as Wernicke's disease
 CC and nutritional polyneuropathy, progressive supranuclear palsy, Shy
 CC Drager's syndrome, multistem degeneration and olivo ponto cerebellar
 CC atrophy, peripheral nerve damage, trauma, and ischaemia resulting from
 CC stroke

XX

SQ Sequence 340 AA;

Query Match 74.6%; Score 1827; DB 2; Length 340;
 Best Local Similarity 99.4%; Pred. No. 3.7e-145;
 Matches 336; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	1	MGPPHSGPGGVRVGALLLLGLVGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL	60
Db	1	MGPPHSGPGGVRVGALLLLGLVGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL	60
Qy	61	LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRDLRFTIKFQEY	120
Db	61	LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRDLRFTIKFQEY	120
Qy	121	SPNLWGHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGAVPRKP	180
Db	121	SPNLWGHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLXVGQSPRGGAVPRKP	180
Qy	181	VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL	240
Db	181	VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL	240
Qy	241	GVAGAGGAMCWRRRRRAKPSERHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGG	300
Db	241	GVAGAGGAMCWRRRRRAKPSERHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGG	300
Qy	301	GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPNIIYY	338
Db	301	GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPQNIYY	338

RESULT 8

ABU07846

ID ABU07846 standard; protein; 340 AA.

XX

AC ABU07846;

XX

DT 10-MAY-2003 (first entry)

XX

DE Mouse ephrin-B3 ligand.

XX
 KW Cytostatic; vasodilator; antiinflammatory; cardiant; gene therapy;
 KW ligand-receptor binding modulator; ephrin ligand; angiogenesis;
 KW lymphangiogenesis; aberrant Ephrin-Tie biology; cell growth disorder;
 KW cell migration disorder; cell proliferation disorder; neovascularisation;
 KW ischaemia; infarction; tissue graft; transplant; mouse; ephrin-B3;
 KW tie receptor tyrosine kinase; Eph receptor ligand.
 XX
 OS Mus musculus.
 XX
 PN WO2003004529-A2.
 XX
 PD 16-JAN-2003.
 XX
 PF 02-JUL-2002; 2002WO-IB002524.
 XX
 PR 02-JUL-2001; 2001US-0302960P.
 XX
 PA (LICN) LICENTIA LTD.
 XX
 PI Alitalo K, Kubo H;
 XX
 DR WPI; 2003-210341/20.
 DR N-PSDB; ABX12547.
 XX
 PT Identifying modulators of binding between a Tie receptor tyrosine kinase
 PT and an Ephrin ligand, useful for promoting neovascularization, comprises
 PT contacting a Tie receptor with an Ephrin in the presence of a putative
 PT modulator.
 XX
 PS Disclosure; Page 121-122; 199pp; English.
 XX
 CC The invention describes a method of identifying a modulator of binding
 CC between a Tie receptor tyrosine kinase and an Ephrin ligand. The method
 CC comprises contacting a Tie receptor composition with an Ephrin
 CC composition in the presence and in the absence of a putative modulator
 CC compound, and detecting the binding between Tie receptor and the Ephrin
 CC in the presence and in the absence of the putative modulator. The method
 CC is useful for identifying a modulator of binding between a Tie receptor
 CC tyrosine kinase and an Ephrin ligand. Modulators identified from the
 CC method are useful in modulating angiogenic processes, including
 CC lymphangiogenesis, for treating diseases associated with aberrant Ephrin-
 CC Tie biology, aberrant growth, migration or proliferation of cells that
 CC express a Tie receptor, or for promoting growth of vessel or
 CC neovascularisation (e.g. ischaemic tissue, an infarction, a new or
 CC chronic compound, or a tissue graft or transplant). This is the amino
 CC acid sequence of mouse Ephrin-B3, a member of the Ephrin-B subclass of
 CC ligands that are bound to the membrane via a transmembrane domain and
 CC short cytoplasmic tail and function as Eph receptor ligands
 XX
 SQ Sequence 340 AA;

Query Match 72.3%; Score 1771; DB 6; Length 340;
 Best Local Similarity 95.6%; Pred. No. 1.9e-140;
 Matches 323; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRDL 60

XX
 DT 21-MAY-1996 (first entry)
 XX
 DE Murine hepatoma transmembrane kinase receptor ligand.
 XX
 KW Hepatoma transmembrane kinase; Htk; receptor; ligand; tyrosine kinase;
 KW neurodegenerative disease.
 XX
 OS Mus musculus.
 XX
 PN W09602645-A2.
 XX
 PD 01-FEB-1996.
 XX
 PF 14-JUL-1995; 95WO-US008812.
 XX
 PR 20-JUL-1994; 94US-00277722.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Bennett BD, Matthews W;
 XX
 DR WPI; 1996-105907/11.
 DR N-PSDB; AAT16470.
 XX
 PT Ligand for the hepatoma trans-membrane kinase receptor - useful for
 PT stimulating and inhibiting cells carrying the receptor, e.g. for treating
 PT neuro-degenerative disease.
 XX
 PS Claim 5; Fig 1(A-D); 88pp; English.
 XX
 CC Mouse (AAT16470) and human (AAT16471) Htk ligand which bind to, and
 CC activate, the Htk receptor, have been identified in a variety of tissues
 CC using a soluble Htk-Fc fusion protein. The predicted mol.wt. of the
 CC murine Htk ligand protein following a signal peptide cleavage is 34 kD
 CC with an estimated pI of 8.9. The murine and human ligands show 96%
 CC homology at the amino acid level. The DNA is used to produce recombinant
 CC ligands; for tissue- specific typing (partic. as a marker for breast
 CC cancer) and as a marker for human chromosome 13. The ligands (partic. in
 CC soluble form) are used to activate the tyrosine kinase domain of the Htk
 CC receptor, i.e. to stimulate or inhibit growth, differentiation, and/or
 CC activation of cells contg. the receptor, e.g. treatment of
 CC neurodegenerative diseases, since they are strongly expressed in the
 CC cerebral cortex, hippocampus, striatum and cerebellum. The ligands are
 CC also useful as a control or standard in assays, for generation of
 CC antibodies, as a mol. wt. marker, for growth in vitro of Htk-receptor
 CC positive cells, as research agent, in screening, etc
 XX
 SQ Sequence 336 AA;

Query Match 25.7%; Score 628.5; DB 2; Length 336;
 Best Local Similarity 41.8%; Pred. No. 2.4e-44;
 Matches 137; Conservative 49; Mismatches 129; Indels 13; Gaps 5;

Qy 14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
 | |::| : : |||:||||:| :| | |||||:|:::|: :
 Db 17 GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 73

PT and an Ephrin ligand, useful for promoting neovascularization, comprises
PT contacting a Tie receptor with an Ephrin in the presence of a putative
PT modulator.

XX

PS Example 1; Page 113-114; 199pp; English.

XX

CC The invention describes a method of identifying a modulator of binding
CC between a Tie receptor tyrosine kinase and an Ephrin ligand. The method
CC comprises contacting a Tie receptor composition with an Ephrin
CC composition in the presence and in the absence of a putative modulator
CC compound, and detecting the binding between Tie receptor and the Ephrin
CC in the presence and in the absence of the putative modulator. The method
CC is useful for identifying a modulator of binding between a Tie receptor
CC tyrosine kinase and an Ephrin ligand. Modulators identified from the
CC method are useful in modulating angiogenic processes, including
CC lymphangiogenesis, for treating diseases associated with aberrant Ephrin-
CC Tie biology, aberrant growth, migration or proliferation of cells that
CC express a Tie receptor, or for promoting growth of vessel or
CC neovascularisation (e.g. ischaemic tissue, an infarction, a new or
CC chronic compound, or a tissue graft or transplant). This is the amino
CC acid sequence of mouse Ephrin-B2, a member of the Ephrin-B subclass of
CC ligands that are bound to the membrane via a transmembrane domain and
CC short cytoplasmic tail and function as Eph receptor ligands

XX

SQ Sequence 336 AA;

Query Match 25.6%; Score 626.5; DB 6; Length 336;
Best Local Similarity 41.4%; Pred. No. 3.6e-44;
Matches 137; Conservative 49; Mismatches 126; Indels 19; Gaps 5;

Qy 14 GALLLLGVLGLVSGLSLEPVYWN SANKRFQ AEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
| |::| : : |||:||||:| :| | |||||:|::|: :
Db 17 GLLMVL CRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 73

Qy 74 PNYEFYKLYLVGGAQGRRC EAPPAPNLLLTCDRDLRLFTIKFQEYSPNLWGHEFRSHH 133
||::|:|:| | || || | ||| |:|:|||||:||||| ||: :
Db 74 GQYEYKVMVDKQADRCTIKKENTPLLNCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133

Qy 134 DYYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQ-----SPRGGAVPRKPVSEMPME 187
||||:|:|:| |||: :||| || ||:|:| || | | :| |
Db 134 DYYIISTSNGLSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNHGPTRPELE---A 190

Qy 188 RDRGAHSL EPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGG 247
| : : | : || | : : : | : || | : : :
Db 191 GTNGRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVV 250

Qy 248 AMCWRRRRRAKPSERHPGPGSFGRGSLGLGGGGMGPREAEPGELGIALRGGAADPPF 307
: ||| : :| | : || :|| :| || || |
Db 251 LLLKYRRRHRKHSPQH TTTLSLSTLATPKRGNN---NGSEPSDVIIPLR---TADSVF 303

Qy 308 CPHYEKVSGDYGHPVYIVQDGPPQSPPNIIY 338
|||||||: |||| ||||
Db 304 CPHYEKVSGDYGHPVYIVQEMPQSPANIY 334

XX

XX

DT

XX

XX

XX

XX

FT

FT

FT

FT

XX

PN WO9411384-A1.

XX

PD 26-MAY-1994.

XX

PF 15-NOV-1993; 93WO-US010955.

XX

PR 13-NOV-1992; 92US-00977693.

XX

PA (IMMV) IMMUNEX CORP.

XX

PI Lyman S, Beckmann MP, Baum PR;

XX

DR WPI; 1994-183415/22.

DR N-PSDB; AAQ65486.

XX

PT New DNA encoding ligand for elk tyrosine kinase receptor - also related
PT polypeptides, vectors, antibodies and probes, useful e.g. in studying
PT cell differentiation or growth.

XX

PS Claim 7; Page 30; 35pp; English.

XX

CC The sequence is that of the elk-L protein able to bind elk, a tyrosine
CC kinase receptor. The DNA may be incorporated into vectors which can used
CC to study the role of elk and its ligands in cell growth and
CC differentiation. (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 346 AA;

Query Match 25.4%; Score 623; DB 2; Length 346;
Best Local Similarity 39.2%; Pred. No. 7.4e-44;
Matches 143; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

QY 8 PGGVRVGALLLLGLVGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRDL 61
 || :| |: |: | :||||| |: |: | |: |||||: ||::

Db 4 PGQRWLGKWL VAMVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

QY 62 CPRARPPGPHSSPNYEfyKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
| | | | | | : | | | | | | : : : : : : : : : : : : : :

Db 64 CPRAEAGRP-----Y EYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118
 Qy 122 PNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
 || | ||: ||||| :||:|: ||||: :||| || ||::: || | :
 Db 119 PNYMGLEFKKHHDYITSTNGSLEGLNREGGVCRTMTMKIIMKVGQDPNAVTPQLTT 178
 Qy 182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
 | | | : : || || : | | ||: || :
 Db 179 SRPSKEADNTVKMATQAPGSRGSLGDSGKHETVNQEEKSGP-----GASGGSSGDPD 231
 Qy 237 -----LLLLGVAGAGGA-----MCWRRRRRAKPSES RHPGPSFGRGSSLGL 277
 : | ||| : | : | : : | : |
 Db 232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLKLKRHRKHTQQ-----RAAALSL 282
 Qy 278 ----GGGGMGPREAEPGELGIALRGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
 || | || : : | || : : ||||| ||||| : |||||
 Db 283 STLASPKGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 339
 Qy 334 PNIYY 338
 ||||
 Db 340 ANIYY 344

RESULT 13

AAR91930

ID AAR91930 standard; protein; 346 AA.

XX

AC AAR91930;

XX

DT 25-MAR-2003 (revised)

DT 11-DEC-1996 (first entry)

XX

DE Human cytokine elk-ligand (elk-L).

XX

KW Human; cytokine; elk-ligand; elk-L; tyrosine kinase receptor;

KW neurotrophic; neuroprotective; placenta; radiolabelled probe; treatment;

KW neural tissue; excito-toxicity; injury; disorder; neural culture reagent;

KW immunogenic fragment; antibody.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1. .24

FT /label= sig_peptide

FT Peptide 25. .346

FT /label= mat_peptide

XX

PN US5512457-A.

XX

PD 30-APR-1996.

XX

PF 15-MAR-1994; 94US-00213403.

XX

PR 13-NOV-1992; 92US-00977693.

XX

PA (IMMV) IMMUNEX CORP.

XX

PI Carpenter MK, Lyman S, Beckmann MP, Baum PR;
 XX
 DR WPI; 1996-229866/23.
 DR N-PSDB; AAT28770.
 XX
 PT DNA coding for neurotrophic human elk ligand cytokine - useful as probe
 PT to isolate other elk ligand sequences.
 XX
 PS Claim 1; Col 27-30; 18pp; English.
 XX
 CC The present sequence is the human cytokine elk-ligand (elk-L), which
 CC binds a member of the tyrosine kinase receptor family. Elk-L exhibits
 CC neurotrophic and neuroprotective properties, and has a calculated mol.
 CC wt. 35180 daltons and a pI of 9.006. The elk-L cDNA, isolated from a
 CC human placental cDNA library, can be radiolabelled and used as a probe
 CC for isolating other mammalian elk-L cDNA. Elk-L can be used to treat
 CC neural tissue disorders, partic. excito-toxicity associated injuries or
 CC disorders, and as a neural culture reagent, while immunogenic fragments
 CC of elk-L can be used to generate specific anti-elk-L antibodies. (Updated
 CC on 25-MAR-2003 to correct PF field.)
 XX
 SQ Sequence 346 AA;

Query Match 25.4%; Score 623; DB 2; Length 346;
 Best Local Similarity 39.2%; Pred. No. 7.4e-44;
 Matches 143; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

Qy	8	PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRDL	61
		: : : : : : : : : : : :	
Db	4	PGQRWLKGKWLIVAMVWVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII	63
Qy	62	CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRDLRLFTIKFQEYS	121
		: : : : : : :	
Db	64	CPRAEAGRP-----YEYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS	118
Qy	122	PNLWGHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGA VPRKPV	181
		: : : : : : :	
Db	119	PNYMGLEFKKHHDYITSTSNGLSLEGLNREGGVCRTRTMKIIMKVGQDPNAVTPQLTT	178
Qy	182	SEMPMERDRGAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA----	236
		: : : : : :	
Db	179	SRPSKEADNTVKMATQAPGSRGSLGDSGKHETVQNQEEKSGP-----GASGGSSGDPD	231
Qy	237	-----LLLLGVAGAGGA-----MCWRRRRRAKPSESRRHPGPGSFGRGGS	277
		: : : : : :	
Db	232	GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLKLKRHRKHTQQ-----RAAALS	282
Qy	278	----GGGGMGPREAEPGELGIALRGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP	333
		: : : :	
Db	283	STLASPKGSGTAGTEPSDIIIPLR--TTENNYCPHYEKVSGDYGHPVYIVQEMPQSP	339
Qy	334	PNIIY 338	
Db	340	ANIIY 344	

AAW19249
ID AAW19249. standard; protein; 346 AA.
XX
AC AAW19249;
XX
DT 25-MAR-2003 (revised)
DT 18-AUG-1997 (first entry)
XX
DE Human elk ligand protien.
XX
KW Human; elk; ligand; elk-L; cytokine; testing; measuring; purification;
KW neuroprotection; treatment; diabetic; hereditary; nutritional;
KW neuropathy; neurodegenerative disease; tissue culture.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Peptide 1. .24
FT /label= sig_peptide
FT Peptide 25. .346
FT /label= mat_peptide
XX
PN US5627267-A.
XX
PD 06-MAY-1997.
XX
PF 01-JUN-1995; 95US-00458077.
XX
PR 13-NOV-1992; 92US-00977693.
PR 15-MAR-1994; 94US-00213403.
XX
PA (IMMV) IMMUNEX CORP.
XX
PI Beckmann MP, Lyman S, Baum PR;
XX
DR WPI; 1997-271366/24.
DR N-PSDB; AAT69766.
XX
PT Human elk ligand protein - for diagnostic or therapeutic use, e.g. as
PT neuro-protective agent.
XX
PS Claim 1; Col 29-32; 18pp; English.
XX
CC The present sequence is a human elk ligand (elk-L) protein, which binds
CC elk, has a calculated molecular weight of 35180 and an isoelectric point
CC of 9.006. Elk-L is a cytokine that can be used to test cells for elk
CC expression, measure the biological activity of elk, purify elk by
CC affinity chromatography and as a neuroprotective agent to treat diabetic,
CC hereditary and nutritional neuropathies and neurodegenerative diseases.
CC It may also be added to tissue cultures to prolong the life of neurons.
CC The elk-L cDNA was isolated from a human placental cDNA library, and is
CC present as a cDNA insert in the recombinant vector deposited in strain
CC ATCC 69085. (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 346 AA;

Query Match

25.4%; Score 623; DB 2; Length 346;

Best Local Similarity 39.2%; Pred. No. 7.4e-44;
Matches 143; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

```

Qy      8 PGGVRVGALLLLGLVGLVSGL-----SLEPVYWNSANKRFQAEAGGYVLYPQIGDRLDLL 61
      ||  :|  |:  |:  :  |  :|||  |:|  |  :|  :  |  |:|:|:|:|:|:|:
Db      4 PGQRWLGKWLAMVWVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy     62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRCEAPPAPNLLLTCDRDLRFTIKFQEYS 121
      |||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db     64 CPRAEAGRP-----YEEYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

Qy    122 PNLWGHEFRSHHDYIIATSDGTREGLESLOGGVCLTRGMKVLLRVGQSPRGGA VPRKPV 181
      ||  |  ||:  |||||  :||:|:  |||:  :|||  ||  ||:  ::|||  |  :
Db    119 PNYMGLEFKKHHDYIITSTSNGLSLEGLNREGGVCRTMTMKIIMKVGQDPNAVTPQLTT 178

Qy    182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPSPMPAVAGAAGGLA---- 236
      |  |  |  :  :  ||  ||  :  |  |  |  |  |  |  |  |  |  |  |
Db    179 SRPSKEADNTVKMATQAPGSRGSLGDSGKHETVNQEEKSGP-----GASGGSSGDPD 231

Qy    237 -----LLLLGVAGAGGA-----MCWRRRRRAKPSESRRHPGPGSFGRGGS LGL 277
      :  |  |||  :  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db    232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLKLRKRHRKHTQQ-----RAAALSL 282

Qy    278 -----GGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
      ||  |  ||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db    283 STLASPKGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPFPQSP 339

Qy    334 PNIIY 338
      |||
Db    340 ANIYY 344

```

RESULT 15

AAW36055

ID AAW36055 standard; protein; 346 AA.

XX

AC AAW36055;

XX

DT 06-MAR-1998 (first entry)

XX

DE Human elk-L protein.

XX

KW Human; elk-L; cytokine; ligand; tyrosine kinase receptor; fusion protein;

KW extracellular domain; immunoglobulin; neurological disease.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Peptide 1. .24

FT /note= "signal peptide"

FT Protein 25. .346

FT /note= "mature protein"

FT Domain 25. .237

FT /note= "extracellular domain; this region is used to

FT generate a fusion protein with the Fc portion of the

FT human immunoglobulin G1"

FT Modified-site 139. .141

FT /note= "Asn is N-glycosylated"
 FT Domain 238. .265
 FT /note= "transmembrane domain"
 FT Domain 266. .346
 FT /note= "intracellular domain"
 FT Cleavage-site 266. .267
 FT /note= "KEX2 protease cleavage site"
 FT Cleavage-site 267. .268
 FT /note= "KEX2 protease cleavage site"
 FT Cleavage-site 270. .271
 FT /note= "KEX2 protease cleavage site"
 XX
 PN US5670625-A.
 XX
 PD 23-SEP-1997.
 XX
 PF 02-JUN-1995; 95US-00460741.
 XX
 PR 13-NOV-1992; 92US-00977693.
 PR 15-MAR-1994; 94US-00213403.
 XX
 PA (IMMV) IMMUNEX CORP.
 XX
 PI Beckmann MP, Lyman S, Baum PR;
 XX
 DR WPI; 1997-479524/44.
 DR N-PSDB; AAT97976.
 XX
 PT Soluble fusion proteins of human elk-ligand and Fc immunoglobulin
 PT fragment - and their dimers and oligomers, useful as neuro-protectants
 PT and neurotrophic agents.
 XX
 PS Claim 1; Col 27-30; 18pp; English.
 XX
 CC This is the amino acid sequence of the human elk-L protein, a new
 CC cytokine that is the ligand for the elk tyrosine kinase receptor. The
 CC extracellular domain of the protein (amino acids 1-213) is used to
 CC generate a fusion protein comprising the Fc polypeptide of the human
 CC immunoglobulin G1 (extending from the hinge region to the C-terminus).
 CC The fusion protein (which has the same activities as the natural elk-L
 CC protein) has neuroprotective and neurotrophic activity so is potentially
 CC useful for treating a wide range of neurological diseases
 XX
 SQ Sequence 346 AA;

Query Match 25.4%; Score 623; DB 2; Length 346;
 Best Local Similarity 39.2%; Pred. No. 7.4e-44;
 Matches 143; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

QY 8 PGGVRV GALLLLGVLGLVSGL-----SLEPVYWN SANKRFQAEGGYVLYPQIGDRLDLL 61
 || :| |: |: : | :||| |:| |:| :| |:|:|:|:|:|:
 Db 4 PGQRWL GKWL VAMVVWALCRLATPLAKNLEPVSWSL NPKFLSGKGLVIYPKIGDKLDII 63
 QY 62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDR PDLDLRFTIKFQEYS 121
 |||| | ||:||||| | | ||:|:|:|:|:|:|:|:|:|:
 Db 64 CPRAEAGRP-----YEYYKLYLV RPEQAAACSTVLDPNVLVT CNRPEQEIRFTIKFQEFS 118

Qy 122 PNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
 || | ||: ||||| :||:|: ||||: :||| || ||::: ||| | :
 Db 119 PNYMGLEFKKHHDYIITSTSNGLGLENREGGVCRTRTMKIIMKVGQDPNAVTPPEQLTT 178
 Qy 182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
 | | | : : || || : | | ||: || :
 Db 179 SRPSKEADNTVKMATQAPGSRGSLGSDGKHETVNQEEKSGP-----GASGGSSGDPD 231
 Qy 237 -----LLLLGVAGAGGA-----MCWRRRRRAKPSES RHPGPGSFGRGGS LGL 277
 : | || : | : | | : : | : | |
 Db 232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLKRHRKHTQQ-----RAAALSL 282
 Qy 278 ----GGGGMGPREAEPGELGIALRGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
 || | || : : || : : ||||| ||||| : |||||
 Db 283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 339
 Qy 334 PNIYY 338
 ||||
 Db 340 ANIYY 344

Search completed: September 15, 2004, 12:35:56
 Job time : 107.591 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2004, 12:32:56 ; Search time 27.4717 Seconds
(without alignments)
855.055 Million cell updates/sec

Title: US-10-021-121-2
Perfect score: 2450
Sequence: 1 MGPPHSGPGGVRVGALLLLG.....TLLRQRASVEAEAGQHGPL 455

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query		DB	ID	Description
	Score	Match Length			
1	1837	75.0	340	4	US-09-214-631-3
2	1835	74.9	340	4	US-09-051-994-2
3	628.5	25.7	336	1	US-08-436-044-2
4	628.5	25.7	336	2	US-08-436-054-2
5	628.5	25.7	336	5	PCT-US95-08812-2
6	623	25.4	346	1	US-08-213-403-2
7	623	25.4	346	1	US-08-458-077-2
8	623	25.4	346	1	US-08-460-741-2
9	623	25.4	346	1	US-08-747-240-2
10	623	25.4	346	1	US-08-299-567-6
11	623	25.4	346	4	US-09-039-642B-2

; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-214-631-3

Query Match 75.0%; Score 1837; DB 4; Length 340;
Best Local Similarity 99.7%; Pred. No. 4.3e-146;
Matches 337; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEAGGYVLYPQIGDRLDL	60
Db	1	MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEAGGYVLYPQIGDRLDL	60
Qy	61	LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRPDLDLRFTIKFQEY	120
Db	61	LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRPDLDLRFTIKFQEY	120
Qy	121	SPNLWGHEFRSHHDYIIATSDGTREGLESIQGGVCLTRGMKVLLRVGQSPRGGAVPRKP	180
Db	121	SPNLWGHEFRSHHDYIIATSDGTREGLESIQGGVCLTRGMKVLLRVGQSPRGGAVPRKP	180
Qy	181	VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL	240
Db	181	VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL	240
Qy	241	GVAGAGGAMCWRRRRRAKPSESRRHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGG	300
Db	241	GVAGAGGAMCWRRRRRAKPSESRRHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGG	300
Qy	301	GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPNNIYY	338
Db	301	GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPNNIYY	338

RESULT 2

US-09-051-994-2

; Sequence 2, Application US/09051994A
; Patent No. 6602683
; GENERAL INFORMATION:
; APPLICANT: REGENERON PHARMACEUTICALS, INC.
; TITLE OF INVENTION: BIOLOGICALLY ACTIVE EPH FAMILY LIGANDS
; FILE REFERENCE: REG-341-PCT-US
; CURRENT APPLICATION NUMBER: US/09/051,994A
; CURRENT FILING DATE: 1998-04-24
; EARLIER APPLICATION NUMBER: PCT/US96/17201
; EARLIER FILING DATE: 1996-10-25
; EARLIER APPLICATION NUMBER: 60/007,015
; EARLIER FILING DATE: 1995-10-25
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 340
; TYPE: PRT
; ORGANISM: Homo sapiens

; FEATURE:
; NAME/KEY: site
; LOCATION: (166)
; OTHER INFORMATION: Xaa=Arg or Gln
US-09-051-994-2

Query Match 74.9%; Score 1835; DB 4; Length 340;
Best Local Similarity 99.7%; Pred. No. 6.4e-146;
Matches 337; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
Qy      1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEAGGYVLYPQIGDRDL 60
          |||
Db      1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEAGGYVLYPQIGDRDL 60

Qy     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRCEAPPAPNLLLTCDRDLRFTIKFQEY 120
          |||
Db     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRCEAPPAPNLLLTCDRDLRFTIKFQEY 120

Qy    121 SPNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
          |||
Db    121 SPNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLXVGQSPRGGAVPRKP 180

Qy    181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
          |||
Db    181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy    241 GVAGAGGAMCWRRRRRAKPSERHPGPGSFGRGGS LGLGGGGMGMPREAEPEGELGIALRGG 300
          |||
Db    241 GVAGAGGAMCWRRRRRAKPSERHPGPGSFGRGGS LGLGGGGMGMPREAEPEGELGIALRGG 300

Qy    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
          |||
Db    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
```

RESULT 3

US-08-436-044-2

; Sequence 2, Application US/08436044
; Patent No. 5624899

; GENERAL INFORMATION:

; APPLICANT: Bennett, Brian D.
; APPLICANT: Matthews, William
; TITLE OF INVENTION: HTK LIGAND
; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)

; CURRENT APPLICATION DATA:


```

; TITLE OF INVENTION: HTK LIGAND
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,054
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/277722
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 902D1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-436-054-2

```

```

Query Match          25.7%; Score 628.5; DB 2; Length 336;
Best Local Similarity 41.8%; Pred. No. 8.2e-45;
Matches 137; Conservative 49; Mismatches 129; Indels 13; Gaps 5;

```

```

Qy      14 GALLLLGLVGLVSGLSLEPVYWNNSANKRFQAEAGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
      | |::| : : |||:||||:| :| | |||||:|::|: :
Db      17 GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 73

Qy      74 PNYEFYKLYLVGGAQGRRCAPPAPNLLLTCDRPDLRLRFTIKFQEYSPNLWGHEFRSHH 133
      ||:|:|:| | | || || | || |::|:|||||:| |||| |:::
Db      74 GQYEYKVMVDKQADRCTIKKENTPLLNCRPDQDVKFTIKFQEFSPNLWGLEFQKNK 133

Qy     134 DYYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
      ||||:|:|:| |||::: |||| || ||:|:| || | | | :|
Db     134 DYYIISTSNGLSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN 193

Qy     191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
      | : : | : || | :: : | : || | : :: : :
Db     194 GRSSTTSFVKPNPGSSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVVLLL 253

Qy     251 WRRRRRAKPSESRHPGPGSFGRGSSLGLGGGGMGMPREAEFGELGIALRGGGAADPPFCPH 310

```

```

      ||| : :| | : || :|| :: | || || |||
Db      254 KYRRRHRKHSPQH TTTLSTLATPKRGGNN----NGSEPSDVIPLR---TADSVFCPH 306

Qy      311 YEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
      ||||| : ||||| ||||
Db      307 YEKVSGDYGHPVYIVQEMPPQSPANIYY 334

```

RESULT 5

PCT-US95-08812-2

; Sequence 2, Application PC/TUS9508812

; GENERAL INFORMATION:

; APPLICANT: Genentech, Inc.

; TITLE OF INVENTION: HTK LIGAND

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: patin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US95/08812

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER:

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Lee, Wendy M.

; REGISTRATION NUMBER: 00,000

; REFERENCE/DOCKET NUMBER: 902PCT

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-1994

; TELEFAX: 415/952-9881

; TELEX: 910/371-7168

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 336 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

PCT-US95-08812-2

Query Match 25.7%; Score 628.5; DB 5; Length 336;

Best Local Similarity 41.8%; Pred. No. 8.2e-45;

Matches 137; Conservative 49; Mismatches 129; Indels 13; Gaps 5;

```

Qy      14 GALLLLGVLGLVSGLSLEPVYWN SANKRFQ AEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
      | |::| : : |||:||||:| :| | |||||:|::|: :
Db      17 GLLMVLCRTAISRSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 73

```

Qy	74	PNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRPDLDRFTIKFQEYSPNLWGHEFRSHH	133
Db	74	GQYEYYKVMVDKQADRCTIKKENTPLLNCRPDDQVKFTIKFQEFSPNLWGLEFQKNK	133
Qy	134	DYYIIATSDGTREGLESLOGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR	190
Db	134	DYYIIISTNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN	193
Qy	191	GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC	250
Db	194	GRSSTTSPFVKPNPGSSTDGNSAGHSGNNLLGSEVALFAGIASGCIIFIVIIITLVVLLL	253
Qy	251	WRRRRRAKPSESRHPGPSFGRGGSGLGGGGGMGPRAEPGELGIALRGGGAADPPFCPH	310
Db	254	KYRRRRHRKHSPQHHTTTLSTLATPKRGGNN---NGSEPSDVIIPLR---TADSVFCPH	306
Qy	311	YEKVS GDYGHVPVYIVQDGPPQSPPNIYY	338
Db	307	YEKVS GDYGHVPVYIVQEMPPQSPANIYY	334

RESULT 6

US-08-213-403-2

; Sequence 2, Application US/08213403

; Patent No. 5512457

; GENERAL INFORMATION:

; APPLICANT: Lyman, Stewart D.

; APPLICANT: Beckmann, M. Patricia

; APPLICANT: Baum, Peter R

; APPLICANT: Carpenter, Melissa

; TITLE OF INVENTION: No. 5512457e1 Cytokine Designated elk Ligand

```
; NUMBER OF SEQUENCES: 2
```

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation

```
; STREET: 51 University Street
```

; CITY: Seattle

; STATE: Washington

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

```
; MEDIUM TYPE: Floppy disk
```

```
;      COMPUTER:  Apple Macintosh
```

```
;      OPERATING SYSTEM:  Apple System 7.1
```

; SOFTWARE: Microsoft Word for Apple, Version 5.1a

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/213,403

; FILING DATE: 15-MAR-1994

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/977,693

; FILING DATE: 13-NOV-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: Seese, Kathryn A.

REGISTRATION NUMBER: 32,172

REFERENCE/DOCKET NUMBER: 2807-A

; TELECOMMUNICATION INFORMATION:

TELEPHONE: (206) 587-0430

; TELEFAX: (206) 233-0644
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 346 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-213-403-2

Query Match 25.4%; Score 623; DB 1; Length 346;
 Best Local Similarity 39.2%; Pred. No. 2.5e-44;
 Matches 143; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

```

Qy      8 PGGVRVGALLLLGVLGLVSGL-----SLEPVYWN SANKRFQAEGGYVLYPQIGDRLDLL 61
      ||  :| |: |: : |      :||| |:| |:| : | |:|:|:|:|:|:|
Db      4 PGQRWLKGWL VAMV V WALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy     62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFITIKFQEYS 121
      ||| | | | :|:|:| | | | | | :|:|:|:|:|:|:|:|:|
Db     64 CPRAEAGRP-----YEYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

Qy    122 PNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
      || | |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db    119 PNYMGLEFKKHHDYITSTSNGLSLEGLNREGGVCRTRTMKIIMKVGD PNAVTPEQLTT 178

Qy    182 SEMP MERDRGAAHSLE-PGKENLP GDPTS NATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
      | | | : : || | | : | | | | :|:|:|
Db    179 SRPSKEADNTVKMATQAPGSRGSLGSDGKHETVNQEEKSGP-----GASGSSGDPD 231

Qy    237 -----LLLLGVAGAGGA-----MCWRRRRRAKPSES RHPGPGSFGRGGS LGL 277
      : | | | | : |:| | : : | :| |
Db    232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLL LKLRKRHRKHTQQ-----RAAALSL 282

Qy    278 ----GGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
      || | | | : : | | : :|:|:|:|:|:|:|:|:|:|:|:|:|
Db    283 STLASPKGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 339

Qy    334 PNIYY 338
      ||| |
Db    340 ANIYY 344
  
```

RESULT 7

US-08-458-077-2

; Sequence 2, Application US/08458077
 ; Patent No. 5627267
 ; GENERAL INFORMATION:
 ; APPLICANT: Lyman, Stewart D.
 ; APPLICANT: Beckmann, M. Patricia
 ; APPLICANT: Baum, Peter R
 ; APPLICANT: Carpenter, Melissa
 ; TITLE OF INVENTION: No. 5627267el Cytokine Designated elk Ligand
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Immunex Corporation
 ; STREET: 51 University Street
 ; CITY: Seattle

Qy 278 ----GGGGMGMPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
 || | || :: | || : : ||||| ||||| : |||||
 Db 283 STLASPKGSGTAGTEPSDIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 339
 Qy 334 PNIYY 338
 ||||
 Db 340 ANIYY 344

RESULT 8

US-08-460-741-2

; Sequence 2, Application US/08460741

; Patent No. 5670625

; GENERAL INFORMATION:

; APPLICANT: Lyman, Stewart D.

; APPLICANT: Beckmann, M. Patricia

; APPLICANT: Baum, Peter R

; APPLICANT: Carpenter, Melissa

; TITLE OF INVENTION: No. 5670625el Cytokine Designated elk Ligand

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation

; STREET: 51 University Street

; CITY: Seattle

; STATE: Washington

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Macintosh

; OPERATING SYSTEM: Apple System 7.1

; SOFTWARE: Microsoft Word for Apple, Version 5.1a

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/460,741

; FILING DATE: 02-JUN-1995

; CLASSIFICATION: 530

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/213,403

; FILING DATE: 15-MAR-1994

; APPLICATION NUMBER: US 07/977,693

; FILING DATE: 13-NOV-1992

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; NAME: Seese, Kathryn A.

; REGISTRATION NUMBER: 32,172

; REFERENCE/DOCKET NUMBER: 2807-A

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 587-0430

; TELEFAX: (206) 233-0644

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 346 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-460-741-2

Query Match 25.4%; Score 623; DB 1; Length 346;
 Best Local Similarity 39.2%; Pred. No. 2.5e-44;
 Matches 143; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

```

Qy      8 PGGVRVGALLLLGLVGLVSGL-----SLEPVYWNSANKRFQAEAGGYVLYPQIGDRDL 61
      ||  :| |: |: : |      :||| |:| |:| : | |:|:|:|:|:|:|
Db      4 PGQRWLKWLIVAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy     62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     64 CPRAEAGRP-----Y EYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

Qy    122 PNLWGHEFRSHHDYIIATSDGTREGLESIQGGVCLTRGMKVLLRVGQSPRGGA VPRKPV 181
      || | | |: | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    119 PNYMGLEFKKHHDYITSTSNGLSLEGLNREGGVCRTRTMKIIMKVGQDPNAVTP EQLT 178

Qy    182 SEMP MERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA----- 236
      | | | | : : || | | : | | | | | | | | | | | | | | | | | | | |
Db    179 SRPSKEADNTVKMATQAPGSRGSLGSDSGKHETV NQEEKSGP-----GASGGSSGDPD 231

Qy    237 -----LLLLGVAGAGGA-----MCWRRRRRAKPSES RHPGPGSFGRGGS LGL 277
      : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLKLKRKRHRKHTQQ-----RAAALSL 282

Qy    278 ----GGGGMGPREAEPGELGIALRGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    283 STLASPKGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMP P QSP 339

Qy    334 PNIYY 338
      ||| |
Db    340 ANIYY 344
  
```

RESULT 9

US-08-747-240-2

; Sequence 2, Application US/08747240

; Patent No. 5728813

; GENERAL INFORMATION:

; APPLICANT: Lyman, Stewart D.

; APPLICANT: Beckmann, M. Patricia

; APPLICANT: Baum, Peter R

; APPLICANT: Carpenter, Melissa

; TITLE OF INVENTION: No. 5728813el Cytokine Designated elk Ligand

; NUMBER OF SEQUENCES: 2

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation

; STREET: 51 University Street

; CITY: Seattle

; STATE: Washington

; COUNTRY: USA

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Macintosh

; OPERATING SYSTEM: Apple System 7.1

; SOFTWARE: Microsoft Word for Apple, Version 5.1a

; CURRENT APPLICATION DATA:

```

; APPLICATION NUMBER: US/08/747,240
; FILING DATE: 12-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/213,403
; FILING DATE: 15-MAR-1994
; APPLICATION NUMBER: US 07/977,693
; FILING DATE: 13-NOV-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2807-A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 346 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-747-240-2

```

```

Query Match          25.4%; Score 623; DB 1; Length 346;
Best Local Similarity 39.2%; Pred. No. 2.5e-44;
Matches 143; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

```

```

Qy      8 PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEAGGYVLYPQIGDRDL 61
      ||  :| |: |: : | :||| |:| |:| : | |:|:|:|:|:|:
Db      4 PGQRWLKGKWLAMVWVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy     62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPLDLRFTIKFQEYS 121
      ||| | | :|:|:|:| | | | :|:|:|:|:|:|:|:|:|:|:|
Db     64 CPRAEAGRP-----YEYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

Qy    122 PNLWGHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
      || | |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db    119 PNYMGLEFKKHHDYITSTSNGLSLEGLNREGGVCRTRTMKIIMKVGQDPNAVTPQLTT 178

Qy    182 SEMPMERDRGAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
      | | | : : || | | : | | | | :|:|:|:|:|:|:|
Db    179 SRPSKEADNTVKMATQAPGSRGSLGSDGKHETVNQEEKSGP-----GASGGSSGDPD 231

Qy    237 -----LLLLGVAGAGGA-----MCWRRRRRAKPSES RHPGPGSFGRGGS LGL 277
      : | | | : |:| | :|:| | :| | :| |
Db    232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLLKLRKRHRKHTQQ-----RAAALSL 282

Qy    278 ----GGGGMGPREAEPGELGIALRGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
      || | | : : | | : :|:|:|:|:|:|:|:|:|:|:|:|:|
Db    283 STLASPKGGSGTAGTEPSDIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPQSP 339

Qy    334 PNIYY 338
      ||| |
Db    340 ANIYY 344

```

RESULT 10
 US-08-299-567-6
 ; Sequence 6, Application US/08299567
 ; Patent No. 5747033
 ; GENERAL INFORMATION:
 ; APPLICANT: Davis, et al.
 ; TITLE OF INVENTION: METHOD OF ENHANCING THE BIOLOGICAL
 ; TITLE OF INVENTION: ACTIVITY OF EPH FAMILY LIGANDS
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Regeneron Pharmaceuticals, Inc.
 ; STREET: 777 Old Saw Mill River Road
 ; CITY: Tarrytown
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10591-6707
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/299,567
 ; FILING DATE: 01-SEP-1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Kempner, Gail M.
 ; REGISTRATION NUMBER: 32,143
 ; REFERENCE/DOCKET NUMBER: REG 290
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 914-345-7400
 ; TELEFAX: 914-345-7721
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 346 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 US-08-299-567-6

Query Match 25.4%; Score 623; DB:1; Length 346;
 Best Local Similarity 39.2%; Pred. No. 2.5e-44;
 Matches 143; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

QY	8	PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL	61
		: : : : : : : : : : : : : :	
Db	4	PGQRWLKGKWLVA MVVWALCRLATPLAKNLEPVSWSSSLNPKFLSGKGLVIYPKIGDKLDII	63
QY	62	CPRARPPGPHSSPNYEFYKLYLVGGAQGRRC EAPPAPNLLLTCDRPLDLRFTIKFQEYS	121
		: : : : : : : : : : : : : : : :	
Db	64	CPRAEAGRP-----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS	118
QY	122	PNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV	181
		: : : : : : : : : : : : : : : : : :	
Db	119	PNYMGLEFKKHHDYIITSTNGSLEGLNREGGVCRTRTMKIIMKVGQDPNAVTPPEQLTT	178

Qy	182	SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA----	236
		: : : : :	
Db	179	SRPSKEADNTVKMATQAPGSRGSLGDSDGKHETVQNQEEKSGP-----GASGGSSGDPD	231
Qy	237	-----LLLLGVAGAGGA-----MCWRRRRRAKPSESRHGPGGSFGRGGSGLGL	277
		: : : : : :	
Db	232	GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLKLKRHRKHTQQ-----RAAALSL	282
Qy	278	----GGGGMGPREAEPGELGIALRGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP	333
		: : : : :	
Db	283	STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP	339
Qy	334	PNIYY	338
Db	340	ANIYY	344

RESULT 11

```

US-09-039-642B-2
; Sequence 2, Application US/09039642B
; Patent No. 6540992
; GENERAL INFORMATION:
; APPLICANT: Lyman, Stewart D.
; APPLICANT: Beckmann, M. Patricia
; APPLICANT: Baum, Peter R.
; APPLICANT: Carpenter, Melissa K.
; TITLE OF INVENTION: NOVEL CYTOKINE DESIGNATED ELK LIGAND
; FILE REFERENCE: GENENT.67CPDV3
; CURRENT APPLICATION NUMBER: US/09/039,642B
; CURRENT FILING DATE: 1998-03-16
; PRIOR APPLICATION NUMBER: 08/213,403
; PRIOR FILING DATE: 1994-03-15
; PRIOR APPLICATION NUMBER: 07/977,693
; PRIOR FILING DATE: 1992-11-13
; PRIOR APPLICATION NUMBER: 08/747,240
; PRIOR FILING DATE: 1996-10-12
; PRIOR APPLICATION NUMBER: 08/460,741
; PRIOR FILING DATE: 1995-06-02
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-039-642B-2

```

Query Match 25.4%; Score 623; DB 4; Length 346;
Best Local Similarity 39.2%; Pred. No. 2.5e-44;
Matches 143; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

QY 8 PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRDL 61
 || :| |: |: :| :||| |:| |:| :| |:|:|:|:|:|:|
 Db 4 PGQRWL GKWL VAMV WALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

QY 62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRC EAPPAPNLLLTCDRPDLDRFTIKFQEYS 121
 |||| | ||:||||| | | ||:|:|:|:|:|:|:|:|:|:|
 Db 64 CPRAEAGRP-----Y EYKLYLV RPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

Qy 122 PNLWGHEFRSHHDYIIATSDGTREGLESLOGGVCLTRGMKVLLRVGQSPRGGA VPRKPV 181
 || | ||: ||||| :||:|: ||||: :||| || ||:::|||| | :
 Db 119 PNYMGLEFKKHHDYITSTSNGLSLEGLNREGGVCRTTRTMKIIMKVGQDPNAVTPQLTT 178
 Qy 182 SEMPMERDRGAHSL- PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
 | | | : : || | | : | | | ||:| | :
 Db 179 SRPSKEADNTVKMATQAPGSRGSLGSDGKHETVNQEEKSGP-----GASGGSSGDPD 231
 Qy 237 -----LLLLGVAGAGGA-----MCWRRRRRAKPSERHPGPGSFGRGGS LGL 277
 : | || | : | | | : : | : |
 Db 232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLRKRRKHTQQ-----RAAALSL 282
 Qy 278 ----GGGGMGPREAEPGELGIALRGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
 || | || : : | || : : ||||| ||||| : |||||
 Db 283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPQSP 339
 Qy 334 PNIYY 338
 ||||
 Db 340 ANIYY 344

RESULT 12

US-08-436-044-4

; Sequence 4, Application US/08436044

; Patent No. 5624899

; GENERAL INFORMATION:

; APPLICANT: Bennett, Brian D.

; APPLICANT: Matthews, William

; TITLE OF INVENTION: HTK LIGAND

; NUMBER OF SEQUENCES: 7

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 460 Point San Bruno Blvd

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: patin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/436,044

; FILING DATE: 05-MAY-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/277722

; FILING DATE: 20-JUL-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Lee, Wendy M.

; REGISTRATION NUMBER: 00,000

; REFERENCE/DOCKET NUMBER: 902D3

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415/225-1994

; TELEFAX: 415/952-9881

```

; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```



```

;   SOFTWARE:  patin (Genentech)
;   CURRENT APPLICATION DATA:
;     APPLICATION NUMBER:  US/08/436,054
;     FILING DATE:  05-MAY-1995
;     CLASSIFICATION:  435
;   PRIOR APPLICATION DATA:
;     APPLICATION NUMBER:  08/277722
;     FILING DATE:  20-JUL-1994
;   ATTORNEY/AGENT INFORMATION:
;     NAME:  Lee, Wendy M.
;     REGISTRATION NUMBER:  00,000
;     REFERENCE/DOCKET NUMBER:  902D1
;   TELECOMMUNICATION INFORMATION:
;     TELEPHONE:  415/225-1994
;     TELEFAX:  415/952-9881
;     TELEX:  910/371-7168
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  333 amino acids
;       TYPE:  amino acid
;       TOPOLOGY:  linear
US-08-436-054-4

```

```

Query Match          25.3%;  Score 620.5;  DB 2;  Length 333;
Best Local Similarity 40.5%;  Pred. No. 3.8e-44;
Matches 133;  Conservative 52;  Mismatches 130;  Indels 13;  Gaps 5;

```

```

Qy      14 GALLLLGLVGLVSGLSLEPVYWN SANKRFQAE GGYVLYPQIGDRLLDLCPRARPPGPHSS 73
      | |::| : : |||:||||:| :| | |||||:|::|: :
Db      14 GVLMLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70

Qy      74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRF TIKFQEYSPNLWGHEFRSHH 133
      ||::|:|:| | || || | :|| |:|||||:|:| ||| |:::
Db      71 GQYEYYKVYMVMDKDQADRCTIKKENTPLL NCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130

Qy     134 DYYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
      ||||:|:|:| |::: :||| || ||:|:| || | | : | :|
Db     131 DYYIISTSNGLSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190

Qy     191 GAAHSLEPGKENLPGDPTS NATS RGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
      | : : | : || | : : : : : : || | | : : : :
Db     191 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL 250

Qy     251 WRRRRRAKPSESRHPGPGSFGRGGS LGLGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
      ||| : :| | : | : || :| :| :| || || |||
Db     251 KYRRRRHRKHSPQH TTTLSLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVFCPH 303

Qy     311 YEKVSGDYGHPVYIVQDGPPQSPPNIIY 338
      |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db     304 YEKVSGDYGHPVYIVQEMPPQSPANIIY 331

```

```

RESULT 14
US-08-271-948-2
; Sequence 2, Application US/08271948
; Patent No. 6303769
; GENERAL INFORMATION:

```

```

; APPLICANT: Cerretti, Douglas P.
; APPLICANT: Reddy, Pranhitha
; TITLE OF INVENTION: No. 6303769e1 Cytokine Designated Lerk-5
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/271,948
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2823
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 333 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-271-948-2

```

```

Query Match          25.3%; Score 620.5; DB 4; Length 333;
Best Local Similarity 40.5%; Pred. No. 3.8e-44;
Matches 133; Conservative 52; Mismatches 130; Indels 13; Gaps 5;

```

```

QY      14 GALLLLGVLGLVSGLSLEPVYWN SANKRFQAEAGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
      | |::| : : ||::|||::| :| | |||||::|::|::| :
Db      14 GVLMLVCRTAISK SIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70

QY      74 PNYEFYKLYLVGGAQGRRC EAPPAPNLLLTCDRPDLRLRFTIKFQEYSPNLWGHEFRSHH 133
      ||::|::| | || || | :|| |::| |||||::| ||||| ||: :
Db      71 GQYEYYKVYMVVDKDQADRCTIKKENTPLL NCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130

QY     134 DYYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
      |||||::|::| ||::| :||| || ||::|::| | | : | :|
Db     131 DYYIIISTNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190

QY     191 GAAHSLEPGKENLPGDPTS NATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
      | : : | : || | :: : : : : || | | : :: : :
Db     191 GRSSTTSPFVKPNPGSS TDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL 250

QY     251 WRRRRRAKPSES RHPGPGSFGRGGS LGLGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310

```

```

Db      251 KYRRHRKHSPOHTTTLSTLATPKRSGNN---NGSEPSDIIPLR---TADSVFCPH 303
Qy      311 YEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
          |||||
Db      304 YEKVSGDYGHPVYIVQEMPQSPANIYY 331

```

RESULT 15

US-08-739-333-2

; Sequence 2, Application US/08739333

; Patent No. 6479459

; GENERAL INFORMATION:

; APPLICANT: Cerretti, Douglas P.

; APPLICANT: Reddy, Pranhitha

; TITLE OF INVENTION: No. 6479459el Cytokine Designated Lerk-5

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation

; STREET: 51 University Street

; CITY: Seattle

; STATE: Washington

; COUNTRY: US

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Macintosh

; OPERATING SYSTEM: Apple 7.1

; SOFTWARE: Microsoft Word, Version 5.1a

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/739,333

; FILING DATE: 29-OCT-1996

; CLASSIFICATION: 536

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/271,948

; FILING DATE: 08-JUL-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Seese, Kathryn A.

; REGISTRATION NUMBER: 32,172

; REFERENCE/DOCKET NUMBER: 2823

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 587-0430

; TELEFAX: (206) 233-0644

; TELEX: 756822

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 333 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-739-333-2

Query Match 25.3%; Score 620.5; DB 4; Length 333;

Best Local Similarity 40.5%; Pred. No. 3.8e-44;

Matches 133; Conservative 52; Mismatches 130; Indels 13; Gaps 5;

Qy 14 GALLLLGVLGLVSGLSLEPVYWSANKRFQAEAGGYVLYPQIGDRDLLCPRARPPGPHSS 73

Db	14	GVLMLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV	70
Qy	74	PNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRDLRFTIKFQEYSPNLWGHEFRSHH	133
Db	71	GQYEEYKVYMVVDKDQADRCTIKKENTPLLNCAPDQDIKFTIKFQEFSPNLWGLEFQKNK	130
Qy	134	DYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR	190
Db	131	DYIIISTSNGLSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN	190
Qy	191	GAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLVAGAGGAMC	250
Db	191	GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL	250
Qy	251	WRRRRAKPSESRRHPGPGSFGRGGSGLGGGGMGPREAEPGELGIALRGGGAADPPFCPH	310
Db	251	KYRRRHRKHSPQHTTTLSLSTLATPKRSGNN---NGSEPSDIIPLR---TADSVFCPH	303
Qy	311	YEKVS GDYGHFVYIVQDGPPQSPPNIYY	338
Db	304	YEKVS GDYGHFVYIVQEMPPQSPANIYY	331

Search completed: September 15, 2004, 12:41:03
Job time : 29.4717 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2004, 12:30:30 ; Search time 29.761 Seconds
(without alignments)
1470.620 Million cell updates/sec

Title: US-10-021-121-2
Perfect score: 2450
Sequence: 1 MGPPHSGPGGVRVGALLLLG.....TTLLRQRASVEAEAGQHGPL 455

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query		DB	ID	Description
	Score	Match Length			
1	628.5	25.7	336	2	I49766
2	623	25.4	346	2	S46993
3	620.5	25.3	333	2	I84743
4	604.5	24.7	345	2	I48780
5	599.5	24.5	345	2	I58406
6	214.5	8.8	237	2	T19914
7	179	7.3	238	2	I38849
8	176	7.2	209	2	A54984
9	175.5	7.2	213	2	JE0322
10	170.5	7.0	228	2	A57084
11	169.5	6.9	201	2	I38850
12	167.5	6.8	228	2	I58170
13	166	6.8	205	2	A36377

14	159	6.5	680	2	S31216	collagen alpha 1(X
15	154.5	6.3	1049	1	CGBO7S	collagen alpha 1(I
16	153.5	6.3	1670	1	CGHU3B	collagen alpha 3(I
17	151.5	6.2	301	2	B31219	collagen 2 - Caeno
18	149	6.1	325	2	T32248	hypothetical prote
19	149	6.1	569	2	S42886	collagen - silkwor
20	148.5	6.1	316	2	T20497	hypothetical prote
21	148	6.0	921	2	S42617	collagen alpha 1(I
22	146.5	6.0	1315	2	A56101	collagen alpha 1(X
23	146.5	6.0	1492	2	A40333	collagen alpha 1'(
24	146.5	6.0	1774	2	B56101	collagen alpha 1(X
25	146	6.0	675	2	S20819	collagen alpha 3(I
26	145.5	5.9	305	2	T20906	hypothetical prote
27	145	5.9	674	2	S13301	collagen alpha 1(X
28	145	5.9	931	2	S13580	collagen alpha 1(I
29	144.5	5.9	438	2	S53787	collagen alpha cha
30	144	5.9	1027	2	S28774	collagen alpha cha
31	143	5.8	1747	2	A54121	collagen alpha-4 c
32	142.5	5.8	635	2	A57131	collagen alpha 2(V
33	142.5	5.8	743	1	S23779	collagen alpha 1(V
34	142.5	5.8	1496	1	CGHU2V	collagen alpha 2(V
35	142	5.8	614	2	T33149	hypothetical prote
36	142	5.8	744	2	S15435	collagen alpha 1(V
37	142	5.8	1029	1	S21369	collagen alpha 2(V
38	142	5.8	1763	2	S16366	collagen alpha 2(I
39	141.5	5.8	1466	1	CGHU7L	collagen alpha 1(I
40	141	5.8	319	2	T32250	hypothetical prote
41	141	5.8	744	1	A34246	collagen alpha 1(V
42	141	5.8	744	1	S23298	collagen alpha 1(V
43	140.5	5.7	305	2	T30165	hypothetical prote
44	140	5.7	304	2	T22482	hypothetical prote
45	140	5.7	680	1	CGHU1D	collagen alpha 1(X

ALIGNMENTS

RESULT 1

I49766

hepatoma transmembrane kinase ligand - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999

C;Accession: I49766

R;Bennett, B.D.; Zeigler, F.C.; Gu, Q.; Fendly, B.; Goddard, A.D.; Gillett, N.; Matthews, W.

Proc. Natl. Acad. Sci. U.S.A. 92, 1866-1870, 1995

A;Title: Molecular cloning of a ligand for the EPH-related receptor protein-tyrosine kinase Htk.

A;Reference number: I49766; MUID:95199254; PMID:7534404

A;Accession: I49766

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-336 <RES>

A;Cross-references: GB:L38847; NID:g769677; PIDN:AAC42052.1; PID:g769678

C;Genetics:

A;Gene: HTK


```

      |||| | ||:|||| | | ||:|:|:|:|:|:|:|:|:|
Db      64 CPRAEAGRP-----Y EYKLYLVLRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEF 118
QY      122 PNLWGHEFRSHHDYIIATSDGTREGLESLOGGVCLTRGMKVLLRVGQSPRGGA VPRKPV 181
      || | ||: ||||| :||:|: ||||: :||| | | ||:::| | | :
Db      119 PNYMGLEFKKHHDYITSTSNGLSLEGLNREGGVCRTMTMKIIMKVGQDPNAVTPQLTT 178
QY      182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
      | | | : : | | | | : | | | | | | | | : | | :
Db      179 SRPSKEADNTVKMATQAPGSRGSLGSDGKHETVNQEEKSGP-----GASGGSSGDPD 231
QY      237 -----LLLLGVAGAGGA-----MCWRRRRRAKPSERHPGPGSFGRGGS LGL 277
      : | | | | : | | | | : | | | | : | | |
Db      232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLKRHRKHTQQ-----RAAALSL 282
QY      278 ----GGGGMGPREAEPGELGIALRGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
      || | | | : : | | | : : ||||| | | | | | | | | | | | | | |
Db      283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 339
QY      334 PNIYY 338
      ||||
Db      340 ANIYY 344

```

RESULT 3

I84743

hepatoma transmembrane kinase ligand - human

C;Species: Homo sapiens (man)

C;Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 05-Nov-1999

C;Accession: I84743

R;Bennett, B.D.; Zeigler, F.C.; Gu, Q.; Fendly, B.; Goddard, A.D.; Gillett, N.; Matthews, W.

Proc. Natl. Acad. Sci. U.S.A. 92, 1866-1870, 1995

A;Title: Molecular cloning of a ligand for the EPH-related receptor protein-tyrosine kinase Htk.

A;Reference number: I49766; MUID:95199254; PMID:7534404

A;Accession: I84743

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-333 <RES>

A;Cross-references: GB:L38734; NID:g769675; PIDN:AAC41752.1; PID:g769676

C;Genetics:

A;Gene: GDB:EPLG5; LERK5

A;Cross-references: GDB:438338; OMIM:600527

A;Map position: 13q33-13q33

Query Match 25.3%; Score 620.5; DB 2; Length 333;

Best Local Similarity 40.5%; Pred. No. 1e-36;

Matches 133; Conservative 52; Mismatches 130; Indels 13; Gaps 5;

```

QY      14 GALLLLGVLGLVSGLSLEPVYWSANKRFQAEGGYVLYPQIGDRDLLCPRARPPGPHSS 73
      | |::| : : |||:||||:| :| | |||||:|:|:|:| :
Db      14 GVLMLCRTAISKSIVLEPIYWSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70
QY      74 PNYEFYKLYLVGGAQGRRC EAPPAPNLLLTCDRPDLRLFTIKFQEYSPNLWGHEFRSHH 133
      ||:|:|:| | | | | | | | | | | | | | | | | | | |
Db      71 GQYEYKVMVDKQADRCTIKKENTPLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130

```


QY 134 DYYIIATSDGTREGLESLOGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
 ||||:|:|:|: |||: :||| || ||:|:| || | | : | :|
 Db 131 DYYIISTNGSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190
 QY 191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
 | : : | : || | : : : : || | | : : : : :
 Db 191 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL 250
 QY 251 WRRRRRAKPSESRHPGPGSFGRRGSLGLGGGGMGMPREAEPEGELGIALRGGAADPPFCPH 310
 ||| : :| | : | : || : : | || || |||
 Db 251 KYRRRHRKHSPQHTTTLSLSTLATPKRSGNN---NGSEPSDIIPLR---TADSVFCPH 303
 QY 311 YEKVSGDYGHPVYIVQDGPPQSPNIIY 338
 ||||| ||||| ||||| : |||| ||||
 Db 304 YEKVSGDYGHPVYIVQEMPQSPANIIY 331

RESULT 4

I48780

Stral/Eplg2 protein - mouse

C;Species: Mus musculus (house mouse)

C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999

C;Accession: I48780; A55507; A55062; S52670

R;Bouillet, P.; Oulad-Abdelghani, M.; Vicaire, S.; Garnier, J.M.; Schuhbaur, B.; Dolle, P.; Chambon, P.

Dev. Biol. 170, 420-433, 1995

A;Title: Efficient cloning of cDNAs of retinoic acid-responsive genes in P19 embryonal carcinoma cells and characterization of a novel mouse gene, Stral (mouse LERK-2/Eplg2).

A;Reference number: I48780; MUID:95377533; PMID:7649373

A;Accession: I48780

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-345 <RES>

A;Cross-references: EMBL:Z48781; NID:g747858; PIDN:CAA88695.1; PID:g747859

R;Fletcher, F.A.; Renshaw, B.; Hollingsworth, T.; Baum, P.; Lyman, S.D.; Jenkins, N.A.; Gilbert, D.J.; Copeland, N.G.; Davison, B.L.

Genomics 24, 127-132, 1994

A;Title: Genomic organization and chromosomal localization of mouse Eplg2, a gene encoding a binding protein for the receptor tyrosine kinase Elk.

A;Reference number: A55507; MUID:95203867; PMID:7896266

A;Accession: A55507

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-345 <FLE>

A;Cross-references: GB:U07598

R;Shao, H.; Lou, L.; Pandey, A.; Pasquale, E.B.; Dixit, V.M.

J. Biol. Chem. 269, 26606-26609, 1994

A;Title: cDNA cloning and characterization of a ligand for the Cek5 receptor protein-tyrosine kinase.

A;Reference number: A55062; MUID:95014510; PMID:7929389

A;Accession: A55062

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-89, 'T', 91-345 <SHA>

A;Cross-references: GB:U12983; NID:g575928; PIDN:AAA53231.1; PID:g575929

C;Genetics:
A;Gene: EPLG2

Query Match 24.7%; Score 604.5; DB 2; Length 345;
Best Local Similarity 37.9%; Pred. No. 1.5e-35;
Matches 136; Conservative 51; Mismatches 107; Indels 65; Gaps 10;

```
QY      15 ALLLLGVLGLVSGL--SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHS 72
      |::| : | : | :||| |:| | : | |::|::|::|::|::| |
Db      15 AMVVLTLCLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDIICPRAEAGRP-- 72

QY      73 SPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRDLRLFTIKFQEYSPNLWGHEFRSH 132
      ||:||||| | | ||::|::| :|||::|::| | ||: :
Db      73 ---YEYYKLYLVRPEQAAACSTVLDPNVLTCKNPKHQEIRFTIKFQEYSPNYMGLEFKKY 129

QY     133 HDYIIIATSDGTREGLESQGVCVCLTRGMKVLLRVGQSPRGGA VPRKPVSEMPMERDRGA 192
      |||| :||::| ||::| :||| || ||:::| | | : : | :
Db     130 HDYYITSTSNGLSLEGLNREGGVCRTRTMKIVMKVGQDP-NAVTPEQLTTSRPSKESDNT 188

QY     193 AHSLEPGKENLPGDPTSNATSRGAEGP-----LPPPSMPAVAGAAGG-----LA 236
      : : | ||::| | | | |
Db     189 VKT-----ATQAPGRGSQGDSDGKHETVNQEEKSGPGAGGGGSGDSDFSFFNSK 236

QY     237 LLLLG VAGAGGA-----MCWRRRRRAKPSES RHPGPGSFGRGGS LGL----GG 279
      : | || | : | | : | : | : |
Db     237 VALFAAVGAGCVIFLLIIIFLTVLLKLRKRHRKHTQQ-----RAAALSSTLSP 287

QY     280 GGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
      || | || : | || : : |||::|::|::|::|::|::|::|::|::|::|::|::|
Db     288 KGGSGTAGTEPSDIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSPANIYY 343
```

RESULT 5

I58406

LERK-2 - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 05-Nov-1999

C;Accession: I58406

R;Fletcher, F.A.; Carpenter, M.; Shilling, H.; Baum, P.; Ziegler, S.; Gimpel, S.; Hollingsworth, T.; VandenBos, T.; Davison, B.L.; Lyman, S.D.; Beckmann, M.P. Oncogene 9, 3241-3248, 1994

A;Title: LERK-2, a ligand for the receptor tyrosine kinase ELK, is evolutionarily conserved and expressed in a developmentally regulated pattern.

A;Reference number: I58406; MUID:95022634; PMID:7936648

A;Accession: I58406

A;Status: preliminary; translated from GB/EMBL/EDBJ

A;Molecule type: mRNA

A;Residues: 1-345 <RES>

A;Cross-references: EMBL:U07560; NID:g563118; PIDN:AAA53092.1; PID:g563119

C;Genetics:

A;Gene: Eplg2

Query Match 24.5%; Score 599.5; DB 2; Length 345;
Best Local Similarity 37.6%; Pred. No. 3.3e-35;
Matches 135; Conservative 52; Mismatches 107; Indels 65; Gaps 10;

```
QY      15 ALLLLGVLGLVSGL--SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHS 72
```

```

      |::| : | : | :||| :| | : | :|::|::|::|::|::|
Db      15 AMVVLTLCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDIICPRAEAGRP-- 72
QY      73 SPNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRDLRLRFTIKFQEYSPNLWGHEFRSH 132
      ||:||||| | | ||::|::| :|||::|::| | ||: :
Db      73 ---YEYKLYLVLRPEQAAACSTVLDPNVLVTCNKPQQEIRFTIKFQEFSPPNYMGLEFKKY 129
QY      133 HDYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGAVPKRPVSEMPMERDRGA 192
      |||| :|::| :||: :||| | | |:::| | | : : | :
Db      130 HDYIITSTSNGLSLEGLNREGGVCRTRTMKIVMKVGQDP-NAVTPQEQLTTSRPSKESDNT 188
QY      193 AHSLEPGKENLPGDPTSNATSRGAEGP-----LPPSPMPAVAGAAGG-----LA 236
      : : | ||::| | | | : |
Db      189 VKT-----ATQAPGRGSQGSDGKHETVNQQEKGSGPGAGSGSGDTSFFNSK 236
QY      237 LLLLGAVAGAGGA-----MCWRRRRRAKPSERHPGPGSFGSGSLGL----GG 279
      : | ||| : | | | : : | : |
Db      237 VALFAAVGAGCVIFLLIIIFLTVLLLLKLRKRHRKHTQQ-----RAAALSLSTLASP 287
QY      280 GGGMGPREAEPGELGIALRGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPNIIYY 338
      | | || :| | | : :|||::|::|::|::|::|::|::|::|
Db      288 KGDSGTAGTEPSDIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSPANIIYY 343

```

RESULT 6

T19914

hypothetical protein C43F9.8 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C;Accession: T19914

R;Mortimore, B.

submitted to the EMBL Data Library, November 1996

A;Reference number: Z19195

A;Accession: T19914

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-237 <WIL>

A;Cross-references: EMBL:Z82262; PIDN:CAB54195.1; GSPDB:GN00022; CESP:C43F9.8

A;Experimental source: clone C43F9

C;Genetics:

A;Gene: CESP:C43F9.8

A;Map position: 4

A;Introns: 32/2; 96/3; 214/1

Query Match 8.8%; Score 214.5; DB 2; Length 237;

Best Local Similarity 25.7%; Pred. No. 3.9e-08;

Matches 53; Conservative 41; Mismatches 83; Indels 29; Gaps 6;

```

QY      11 VRVGALLLLGLVGLVS-GLSLEPVYWNANKRFQAEG-GYVLYPQIGDRDLDCPRARPP 68
      :: :| : : : : | | | :| : |||: : ||::
Db      1 MQIATFILLSLFPFIGWARKIPDINWISSNPIDFVSNTDHVISVHIGDRVSIRCPKSD 60
QY      69 GPHSSPNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRDLRLRFTIKFQEYSPNLWGHE 128
      | ||: :|: | : | | : || : : | | : :| | |
Db      61 G-----KYEYSYIYMVSDEEYDHCFL-SKPRLVGACDNQTINASINIVFRSFTPTPGGFE 114
QY      129 FRSHHDYIIA-----TSDGTREGLESQGGVCLTRGMKVLLRVGQ 169

```

```

      |:  :|::|:  ||||| ||::  : |:|  : ||:  |||
Db      115 FQPGKNYFLISKSEVDALIIYETANQIFPGTSDGTLEGIDRKKDGLCTAKQMKIKFEVGQ 174
QY      170 SPRGGAVPRKPVSEMPMERDRGAAHS 195
      ||  |:  :  ::||| ||
Db      175 DRRGIENPK--FAARTLKKDRDAEHS 198

```

RESULT 7

I38849

LERK-3 - human

C;Species: Homo sapiens (man)

C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 29-Sep-1999

C;Accession: I38849

R;Kozlosky, C.J.; Maraskovsky, E.; McGrew, J.T.; VandenBos, T.; Teepe, M.;
Lyman, S.D.; Srinivasan, S.; Fletcher, F.A.; Gayle, R.B.
Oncogene 10, 299-306, 1995

A;Title: Ligands for the receptor tyrosine kinases hek and elk: isolation of
cDNAs encoding a family of proteins.

A;Reference number: I38849; MUID:95140419; PMID:7838529

A;Accession: I38849

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-238 <RES>

A;Cross-references: EMBL:U14187; NID:g642832; PIDN:AAC50078.1; PID:g642833

C;Genetics:

A;Gene: GDB:EPLG3

A;Cross-references: GDB:438336; OMIM:601381

A;Map position: 1q21-1q22

C;Superfamily: axon guidance signal protein

```

Query Match          7.3%;  Score 179;  DB 2;  Length 238;
Best Local Similarity 28.4%;  Pred. No. 1.3e-05;
Matches 65;  Conservative 24;  Mismatches 80;  Indels 60;  Gaps 12;

```

```

QY      7 GPGGVVRVGALLLLGLVGLVSGLSLEPVYWNSANKRFQAEAGGYVLYPQIGDRLDLLCP--R 64
      |||  |  |  :  |||||::  : |  |  :  |  |  |  |
Db      24 GPG-----GALG-----NRHAVYWNSSNQHLRRE-GYTVQVNVNDYLDIYCPHYN 67

QY      65 ARPPGPHSSP----NYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRPDL---DLRFTIKF 117
      :  ||  : |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      68 SSGVGPGAGPGPGGGAEQYVLYMVSRNGYRTCNASQGFK-RWECNRPHAPHSPIKFSEKF 126

QY      118 QEYSPNLWGHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGAVP 177
      |  |  |  |  |  :  |  |  |  |  |  |  |  |  |  |  |  |  |
Db      127 QRISAFSLGYEFHAGHEYYYISTPTHNLH-----WKCLR--MKVFVCCASTSHSG--- 174

QY      178 RKPVSEMP-----MERDRGAAHSLE-----PGKENLP 204
      |||  :|  |  :  |  |  |  |  |  |  |  |  |  |  |  |
Db      175 EKPVPTLPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLP 223

```

RESULT 8

A54984

ELF-1 protein precursor - mouse

N;Alternate names: Cek7 ligand

C;Species: Mus musculus (house mouse)

C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 29-Sep-1999
 C;Accession: A54984; A55873
 R;Cheng, H.J.; Flanagan, J.G.
 Cell 79, 157-168, 1994
 A;Title: Identification and cloning of ELF-1, a developmentally expressed ligand for the Mek4 and Sek receptor tyrosine kinases.
 A;Reference number: A54984; MUID:95007776; PMID:7522971
 A;Accession: A54984
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-209 <CHE>
 A;Cross-references: GB:U14941; NID:g558836; PIDN:AAA53636.1; PID:g558837
 R;Shao, H.; Lou, L.; Pandey, A.; Verderame, M.F.; Siever, D.A.; Dixit, V.M.
 J. Biol. Chem. 270, 3467-3470, 1995
 A;Title: cDNA cloning and characterization of a Cek7 receptor protein-tyrosine kinase ligand that is identical to the ligand (ELF-1) for the Mek-4 and Sek receptor protein-tyrosine kinases.
 A;Reference number: A55873; MUID:95181289; PMID:7876076
 A;Accession: A55873
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-209 <SHA>
 A;Cross-references: GB:U14752; NID:g681886; PIDN:AAA68520.1; PID:g681887
 C;Superfamily: axon guidance signal protein
 C;Keywords: lipoprotein; membrane protein

Query Match 7.2%; Score 176; DB 2; Length 209;
 Best Local Similarity 29.3%; Pred. No. 1.8e-05;
 Matches 58; Conservative 19; Mismatches 69; Indels 52; Gaps 7;

```

Qy      33 VYWNSANKRFQAE-----GGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGA 87
      |||| :| |||      ||| :  | | ||: ||  | | :  | | ||:| |
Db      35 VYWNRSNPRFQVSAVGDDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMERYILYMVNGE 93

Qy      88 QGRRCEAPPAPNLLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHDYIIATSDGT 144
      |:      |:|      |:|: ||| :|  | ||| |:| |: :
Db      94 GHASCDHRQRGFKRWE CNRPAAPGGPLKFSEKFQLFTPFSLGFEPGHEYYYYISATP-- 151

Qy     145 REGLES LQGGVCLTRGMKVLLRVGQSPRGGA VPRKPVSEMPMERDRGAAHSLEPGKENLP 204
      :|      ||      :|| :|  | | |
Db     152 ----PNLVDRPCLR--LKVYVR-----PTNETLY 174

Qy     205 GDP----TSNATSRGAEG 218
      |      |||: :  | |
Db     175 EAPEPIFTSNSSCSGLGG 192

```

RESULT 9

JE0322

ephrin-A2 - human

C;Species: Homo sapiens (man)

C;Date: 05-Feb-1999 #sequence_revision 05-Feb-1999 #text_change 21-Jul-2000

C;Accession: JE0322

R;Aasheim, H.; Pedoutour, F.; Grosgeorge, J.; Logtenberg, T.

Biochem. Biophys. Res. Commun. 252, 378-382, 1998

A;Title: Cloning, chromosomal mapping, and tissue expression of the gene encoding the human Eph-family kinase ligand ephrin-A2.

A;Reference number: JE0322; MUID:99045414; PMID:9826538
 A;Accession: JE0322
 A;Status: preliminary
 A;Molecule type: mRNA
 A;Residues: 1-213 <AAS>
 A;Cross-references: GB:AJ007292; NID:g3688367; PIDN:CAA07435.1; PID:g3688368
 C;Superfamily: axon guidance signal protein

Query Match 7.2%; Score 175.5; DB 2; Length 213;
 Best Local Similarity 36.8%; Pred. No. 2e-05;
 Matches 43; Conservative 14; Mismatches 51; Indels 9; Gaps 3;

QY 33 VYWSANKRFQA-----EGGYVLYPQIGDRLLCPRARPPGPHSSPNYEFYKLYLVGGA 87
 |||| :| || | ||| : | | ||: || | | : | | ||:| |
 Db 39 VYWNRSNPRFHAGAGDDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMEHYVLYMVNGE 97
 QY 88 QGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHDYIIATS 141
 |: ||| |:| |:| ||| ::| | ||| |:| |:| :
 Db 98 GHASCDHRQRGFKRWEENRPAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISAT 154

RESULT 10

A57084

repulsive axon guidance signal protein RAGS precursor - chicken

C;Species: Gallus gallus (chicken)

C;Date: 03-Nov-1995 #sequence_revision 03-Nov-1995 #text_change 20-Jun-2000

C;Accession: A57084

R;Drescher, U.; Kremoser, C.; Handweker, C.; Loeschinger, J.; Noda, M.;
 Bonhoeffer, F.

Cell 82, 359-370, 1995

A;Title: In vitro guidance of retinal ganglion cell axons by RAGS, a 25 kDa
 tectal protein related to ligands for Eph receptor tyrosine kinases.

A;Reference number: A57084; MUID:95360980; PMID:7634326

A;Accession: A57084

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-228 <DRE>

A;Cross-references: GB:X90377; NID:g1061113; PIDN:CAA62027.1; PID:g984118

C;Superfamily: axon guidance signal protein

C;Keywords: glycoprotein; membrane protein; phosphatidylinositol linkage

F;1-20/Domain: signal sequence #status predicted <SIG>

Query Match 7.0%; Score 170.5; DB 2; Length 228;
 Best Local Similarity 28.9%; Pred. No. 4.8e-05;
 Matches 73; Conservative 30; Mismatches 91; Indels 59; Gaps 13;

QY 16 LLLLGVLGL-VSGLSLEP-----VYWSANKRFQAEGGYVLYPQIGDRLLCPR 64
 :||| | | | || |||| | ||| :| | : | | ||: ||
 Db 6 MLLLAVALWVCVRGQEPGRKAVADRYAVYWNSTNPRFQ-QGDYHIDVCINDYLDVFCPH 64
 QY 65 ARPPGPHSSPNYEFYKLYLVG-----GAQGRRCEAPPAPNLLLTCDRPDLDLR 112
 | | | ||:| | : | | :|| |:
 Db 65 YEDSVPEDKT--ERYVLYMVNFDGYSSCDHISKGFKRWEENRPHSPN-----GPLK 113
 QY 113 FTIKFQEYSPNLWGHEFRSHHDYIIATS---DGTREGLESQGGVCLTRGMKVLLRVGQ 169
 |: ||| ::| | ||| :|: |:| :| | || :|| :|
 Db 114 FSEKFQLFTPFSLGFEFRPGREYFYISSAIPDNGRRS-----CLK--LKVFVR--- 159

```

Qy      170 SPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMP--A 227
      | : | : : : ||| : : | ||| | :|
Db      160 -PANSCMKTIGVHDRVFDVNDKVENSLPADDTV--RESAEPSRG-ENAAQTPRIPIRL 214

Qy      228 VAGAAGGLALLLL 240
      :| ||:|:
Db      215 LATLLFLLAMLLI 227

```

RESULT 11

I38850

LERK-4 - human

C;Species: Homo sapiens (man)

C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text change 29-Sep-1999

C;Accession: I38850

R;Kozlosky, C.J.; Maraskovsky, E.; McGrew, J.T.; VandenBos, T.; Teepe, M.;
Lyman, S.D.; Srinivasan, S.; Fletcher, F.A.; Gayle, R.B.

Oncogene 10, 299-306, 1995

A;Title: Ligands for the receptor tyrosine kinases hek and elk: isolation of cDNAs encoding a family of proteins.

A;Reference number: I38849; MUID:95140419; PMID:7838529

A;Accession: I38850

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-201 <RES>

A;Cross-references: EMBL:U14188; NID:g642834; PIDN:AAC50079.1; PID:g642835

C; Genetics:

A; Gene: GDB:EPLG4

A;Cross-references: GDB:438337; OMIM:601380

A;Map position: 1q21-1q22

C;Superfamily: axon guidance signal protein

Query Match 6.9%; Score 169.5; DB 2; Length 201;
Best Local Similarity 29.9%; Pred. No. 5e-05;
Matches 66; Conservative 18; Mismatches 82; Indels 55; Gaps 10;

QY	24	LVSGLSL-EPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLY	82
		: : : : :	
Db	20	LRGGSSLRHVYWNSSNPRL-LRGDAVVELGLNDYLDIVCPHYEGPGPPEGP--ETFALY	76
QY	83	LVGGAQGRRCEAP-PAPNLLLTCDRPDLRLFTIKFQEYSPNLWGHEFRSHHDYIIATS	141
		: : : : : :	
Db	77	MVDWPGYESCQAEQPRAYKRWVCSLPFGHVQFSEKIQRFTPFSLGFELPGETYYYISVP	136
QY	142	DGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGA VPRKPVSEMPMERDRGAAN SLEPGKE	201
		: :	
Db	137	--TPE-----SSGQCL-----RLQVSVCCKERKSES AHPV-----	164
QY	202	NLPGDPTSNATS--RGAEGPLPPPSMPAVAGAAGGLALLLL	240
		: :	
Db	165	---GSPGESGTSGWRGGDTPSP-----LCLLLL	189

RESULT 12

I58170

LERK-7 precursor - human

N;Alternate names: AL-1
 C;Species: Homo sapiens (man)
 C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 29-Sep-1999
 C;Accession: I58170; G01812
 R;Winslow, J.W.; Moran, P.; Valverde, J.; Shih, A.; Yuan, J.Q.; Wong, S.C.;
 Tsai, S.P.; Goddard, A.; Henzel, W.J.; Hefti, F.
 Neuron 14, 973-981, 1995
 A;Title: Cloning of AL-1, a ligand for an Eph-related tyrosine kinase receptor
 involved in axon bundle formation.
 A;Reference number: I58170; MUID:95267434; PMID:7748564
 A;Accession: I58170
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-228 <RES>
 A;Cross-references: GB:S77167; NID:g914184; PID:g914185
 R;Kozlosky, C.J.; VandenBos, T.; Park, L.S.; Cerretti, D.P.; Carpenter, M.K.
 submitted to the EMBL Data Library, May 1995
 A;Reference number: G08477
 A;Accession: G01812
 A;Status: preliminary; translated from GB/EMBL/DDBJ
 A;Molecule type: mRNA
 A;Residues: 1-228 <KOZ>
 A;Cross-references: EMBL:U26403; NID:g1019430; PIDN:AAB60377.1; PID:g1019431
 C;Genetics:
 A;Gene: GDB:EPLG7; AF1; LERK7
 A;Cross-references: GDB:568757; OMIM:601535
 A;Map position: 13q33-13q33
 C;Superfamily: axon guidance signal protein

Query Match 6.8%; Score 167.5; DB 2; Length 228;
 Best Local Similarity 28.8%; Pred. No. 7.9e-05;
 Matches 65; Conservative 29; Mismatches 81; Indels 51; Gaps 11;

```

Qy      33 VYWNSANKRFQAEAGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVG----- 85
        |||||:| ||| | | : | | ||: || | | | | :|
Db      34 VYWNSSNPRFQ-RGDYHIDVCINDYLDVFCPHYEDSVPEDKT--ERYVLYMVNFDGYSAC 90

Qy      86 -----GAQGRRCCEAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLWGHEFRSHHDYIIAT 140
        | : | | :|| | :| ||| :| | || | :| :|
Db      91 DHTSKGFKRWECNRPHSPN-----GPLKFSEKFQLFTPFSLGFEFRPGREYFYISS 141

Qy      141 S---DGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAHSLE 197
        : :| | | | | :|| :| | : | : | : : :|||
Db      142 AIPDNRRS-----CLK--LKVFVR----PTNSCMKTIGVHDRVFDVNDKVENSL 186

Qy      198 PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGCLALLLLGVA 243
        | : : | ||| | | :| : ||| :|
Db      187 PADDTV---HESAEPSRG-ENAAQTPRIPSRL-----LAILLFLLA 223

```

RESULT 13

A36377

B61 protein precursor - human

C;Species: Homo sapiens (man)

C;Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 29-Sep-1999

C;Accession: A36377

R;Holzman, L.B.; Marks, R.M.; Dixit, V.M.

Mol. Cell. Biol. 10, 5830-5838, 1990

A;Title: A novel immediate-early response gene of endothelium is induced by cytokines and encodes a secreted protein.

A;Reference number: A36377; MUID:91042512; PMID:2233719

A;Accession: A36377

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-205 <HOL>

A;Cross-references: GB:M57730; GB:M37476; NID:g179320; PIDN:AAA58388.1; PID:g179321

C;Superfamily: axon guidance signal protein

Query Match 6.8%; Score 166; DB 2; Length 205;
Best Local Similarity 27.5%; Pred. No. 9e-05;
Matches 46; Conservative 31; Mismatches 74; Indels 16; Gaps 5;

```
QY      18 LLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRDLLCPRARPPGPHSSPN-- 75
      |||:  ::  |:|||:| :|: | | :: |: | :|::||  || :
Db       8 LLGLCCSLAAADRHTVFWNSSNPKEFNE-DYTIHVQLNDYVDIICPHYE---DHSVADAA 63

QY      76 YEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSH 132
      | | ||||  : : |:  : |:||  : : ||| ::| | ||:
Db      64 MEQYILYLVEHEEYQLCQPQSKDQVRWQCNRPSAKHGPEKLSEKFQRFPTFTLGKEFKEG 123

QY     133 HDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVPRK 179
      | || |:  |  ||  : | :: ||:  |::
Db     124 HSYYYISKPIHQHEDR-----CLRLKVTVSGKITHSPQAHVNPQE 163
```

RESULT 14

S31216

collagen alpha 1(X) chain precursor - mouse

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 13-Aug-1999

C;Accession: S31216; S28807; S22215; S30127; I48299; S26397; S31830

R;Kong, R.Y.C.; Kwan, K.M.; Lau, E.T.; Thomas, J.T.; Boot-Handford, R.P.; Grant, M.E.; Cheah, K.S.E.

Eur. J. Biochem. 213, 99-111, 1993

A;Title: Intron-exon structure, alternative use of promoter and expression of the mouse collagen X gene, Coll10a-1.

A;Reference number: S31216; MUID:93238750; PMID:8477738

A;Accession: S31216

A;Molecule type: DNA

A;Residues: 1-680 <KON>

A;Cross-references: EMBL:Z21610; NID:g49793; PIDN:CAA79736.1; PID:g49794

R;Elima, K.; Eerola, I.; Rosati, R.; Metsaeranta, M.; Garofalo, S.; Peraelae, M.; de Crombrughe, B.; Vuorio, E.

Biochem. J. 289, 247-253, 1993

A;Title: The mouse collagen X gene: complete nucleotide sequence, exon structure and expression pattern.

A;Reference number: S28807; MUID:93143676; PMID:8424763

A;Accession: S28807

A;Molecule type: DNA

A;Residues: 1-285, 'A', 287-680 <ELI>

A;Cross-references: EMBL:X67348; NID:g50480; PIDN:CAA47763.1; PID:g50481

R;Elima, K.; Metsaeranta, M.; Kallio, J.; Peraelae, M.; Eerola, I.; Garofalo, S.; de Crombrughe, B.; Vuorio, E.

Biochim. Biophys. Acta 1130, 78-80, 1992
A;Title: Specific hybridization probes for mouse alpha-2(IX) and alpha-1(X) collagen mRNAs.
A;Reference number: S22215; MUID:92182017; PMID:1543751
A;Accession: S22215
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 385-450, 'K', 452-627 <ELA>
A;Cross-references: EMBL:X63013; NID:g49795; PIDN:CAA44741.1; PID:g49796
R;Apte, S.S.; Olsen, B.R.
Matrix 13, 165-179, 1993
A;Title: Characterization of the mouse type X collagen gene.
A;Reference number: S30127; MUID:93261348; PMID:8492743
A;Accession: S30127
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-12, 'F', 14-26, 'S', 28-247, 'L', 249-285, 'A', 287-305, 'F', 307-416, 'S', 418-499, 'L', 501-566, 'C', 568, 'H', 570, 'IY', 573-634, 'T', 636-680 <APT>
R;Apte, S.S.; Seldin, M.F.; Hayashi, M.; Olsen, B.R.
Eur. J. Biochem. 206, 217-224, 1992
A;Title: Cloning of the human and mouse type X collagen genes and mapping of the mouse type X collagen gene to chromosome 10.
A;Reference number: I48299; MUID:92267014; PMID:1587271
A;Accession: I48299
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 52-247, 'L', 249-285, 'A', 287-305, 'F', 307-416, 'S', 418-499, 'L', 501-566, 'C', 568, 'H', 570, 'IY', 573-634, 'T', 636-680 <RES>
A;Cross-references: EMBL:X65121; NID:g50482; PIDN:CAA46237.1; PID:g667031
R;Summers, T.A.; Irwin, M.H.; Mayne, R.; Balian, G.
J. Biol. Chem. 263, 581-587, 1988
A;Title: Monoclonal antibodies to type X collagen. Biosynthetic studies using an antibody to the amino-terminal domain.
A;Reference number: S26397; MUID:88087150; PMID:2826450
A;Accession: S26397
A;Molecule type: protein
A;Residues: 'SDGYFSQ', 24-26, 'KQ' <SUM>
C;Genetics:
A;Gene: Coll10a-1
A;Map position: 10
A;Introns: 51/3
C;Superfamily: collagen alpha 1(VIII) chain; complement C1q carboxyl-terminal homology
C;Keywords: coiled coil; extracellular matrix; glycoprotein; homotrimer
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-680/Product: collagen alpha 1(X) chain #status predicted <MAT>
F;553-679/Domain: complement C1q carboxyl-terminal homology <C1Q>

Query Match 6.5%; Score 159; DB 2; Length 680;
Best Local Similarity 25.5%; Pred. No. 0.0011;
Matches 97; Conservative 30; Mismatches 108; Indels 146; Gaps 24;

QY 1 MGPPHSGPGGV-RVGALLLLGVLGLVSGLSLEPVYWN SANKRFQAEAGGYVLYPQIGDRLD 59
: ||| || || | | | : : : | | |
Db 211 IGPP--GPSGVGRRGENGFPGQPGI-----KGDRGFPGEMG----- 244
QY 60 LLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQE 119

```

      : |||| |      | ||| |      | : : :| :
Db    245 ----PSGPPGPQGPP-----GKQGR--EGIGKPGAIGSPGQPGI----- 277
QY    120 YSPNLWGHEFRSHHDYIIATSDGT---REGLESLOGGVCLTRGMKVLLRVGQSPRGGA 175
      |  ||      || |      :|| | :|      ||      | |
Db    278 --PGEKGHPGSPG-----IAGPPGAPGFGKQGLPGLRG---QRG-----PAG-- 314
QY    176 VPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTSNAISRGAEGPLPPPSMPAVAGAAGGL 235
      :| | :      : :|| |      ||: ||| |      : | :|| |      : || | :
Db    315 LPGAPGA---KGERGPAG--HPGEPGLPGSP---GNMGPQGPKGIPGNHGIPGAKGEI 364
QY    236 ALLLLGVAGAGGAMCWRRRRAKP---SESRRHPG-----PGSFGRGGSLLGLGGGGG 282
      | :| || || | | |      : : ||      || | : | | :|| |
Db    365 G--LVGPAGPPGA---RGARGPPGLDGKTGYPGEPGLNGPKGNPGLPGQKGDPGVGGTPG 419
QY    283 M-----GPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVY 323
      :      ||| ||| |      | || | :      || | :|
Db    420 LRGPVGPVGAKGVPGHNGEAGPR-GEPIPGTR----GPTGPPGVPGFPGSKGDPGNP-- 472
QY    324 IVQDGP-----PQSPP 334
      ||      | ||
Db    473 -GAPGPAGIATKGLNGPTGPP 492

```

RESULT 15

CGBO7S

collagen alpha 1(III) chain - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 07-May-1999

C;Accession: A02862; A38001; A38002; A38003; A38004; A38005; S71946

R;Fietzek, P.P.; Allmann, H.; Rauterberg, J.; Henkel, W.; Wachter, E.; Kuehn, K. Hoppe-Seyler's Z. Physiol. Chem. 360, 809-820, 1979

A;Title: The covalent structure of calf skin type III collagen. I. The amino acid sequence of the amino terminal region of the alpha1(III) chain (position 1-222).

A;Reference number: A02862; MUID:80026026; PMID:488906

A;Accession: A02862

A;Molecule type: protein

A;Residues: 1-242 <FIE>

R;Dewes, H.; Fietzek, P.P.; Kuehn, K.

Hoppe-Seyler's Z. Physiol. Chem. 360, 821-832, 1979

A;Title: The covalent structure of calf skin type III collagen. II. The amino acid sequence of the cyanogen bromide peptide alpha1(III)CB1,8,10,2 (positions 223-402).

A;Reference number: A38001; MUID:80026027; PMID:488907

A;Accession: A38001

A;Molecule type: protein

A;Residues: 243-422 <DEW1>

R;Bentz, H.; Fietzek, P.P.; Kuehn, K.

Hoppe-Seyler's Z. Physiol. Chem. 360, 833-840, 1979

A;Title: The covalent structure of calf skin type III collagen. III. The amino acid sequence of the cyanogen bromide peptide alpha1(III)CB4 (positions 403-551).

A;Reference number: A38002; MUID:80026028; PMID:488908

A;Accession: A38002

A;Molecule type: protein

A;Residues: 423-571 <BEN>

R;Lang, H.; Glanville, R.W.; Fietzek, P.P.; Kuehn, K.
 Hoppe-Seyler's Z. Physiol. Chem. 360, 841-850, 1979
 A;Title: The covalent structure of calf skin type III collagen. IV. The amino
 acid sequence of the cyanogen bromide peptide alphas(III)CB5 (positions 552-
 788).
 A;Reference number: A38003; MUID:80026029; PMID:488909
 A;Accession: A38003
 A;Molecule type: protein
 A;Residues: 572-808 <LAN>
 R;Dewes, H.; Fietzek, P.P.; Kuehn, K.
 Hoppe-Seyler's Z. Physiol. Chem. 360, 851-860, 1979
 A;Title: The covalent structure of calf skin type III collagen. V. The amino
 acid sequence of the cyanogen bromide peptide alphas(III)CB9A (position 789 to
 927).
 A;Reference number: A38004; MUID:80026030; PMID:488910
 A;Accession: A38004
 A;Molecule type: protein
 A;Residues: 809-947 <DEW2>
 R;Allmann, H.; Fietzek, P.P.; Glanville, R.W.; Kuehn, K.
 Hoppe-Seyler's Z. Physiol. Chem. 360, 861-868, 1979
 A;Title: The covalent structure of calf skin type III collagen. VI. The amino
 acid sequence of the carboxyterminal cyanogen bromide peptide alphas(III)CB9B
 (position 928-1028).
 A;Reference number: A38005; MUID:80026031; PMID:488911
 A;Accession: A38005
 A;Molecule type: protein
 A;Residues: 948-1049 <ALL>
 A;Experimental source: skin
 R;Henkel, W.
 Biochem. J. 318, 497-503, 1996
 A;Title: Cross-link analysis of the C-telopeptide domain from type III collagen.
 A;Reference number: S71946; MUID:96404897; PMID:8809038
 A;Accession: S71946
 A;Molecule type: protein
 A;Residues: 87-106;1017-1029;1037-1049 <HEN>
 C;Comment: Prolines at the third position of the tripeptide repeating unit (G-X-
 Y) are hydroxylated in some or all of the chains.
 C;Comment: The type III collagen molecule is a trimer of identical chains,
 linked to each other by interchain disulfide bonds. Trimers are also cross-
 linked by allysines forming desmosine.
 C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal
 homology; von Willebrand factor type C repeat homology
 C;Keywords: coiled coil; extracellular matrix; glycoprotein; hydroxylysine;
 hydroxyproline; skin; trimer; triple helix
 F;1-1049/Product: collagen alpha 1(III) chain #status experimental <CAB>
 F;1-14/Region: amino-terminal nonhelical telopeptide
 F;15-1040/Region: helical
 F;587-589/Region: cell attachment (R-G-D) motif
 F;752-754/Region: cell attachment (R-G-D) motif
 F;875-877/Region: cell attachment (R-G-D) motif
 F;878-880/Region: cell attachment (R-G-D) motif
 F;935-937/Region: cell attachment (R-G-D) motif
 F;1041-1049/Region: carboxyl-terminal nonhelical telopeptide
 F;95,107,119,938,950/Modified site: 5-hydroxylysine (Lys) #status experimental
 F;107/Modified site: allysine (Lys) #status predicted
 F;107/Binding site: carbohydrate (Lys) (covalent) #status experimental
 F;1040,1041/Disulfide bonds: interchain #status predicted

Query Match 6.3%; Score 154.5; DB 1; Length 1049;
 Best Local Similarity 26.5%; Pred. No. 0.0036;
 Matches 60; Conservative 9; Mismatches 74; Indels 83; Gaps 8;

```

Qy      171 PRGGAVPRKPVSEMPMERDRGA-----AHSLEPGKEN 202
      | ||: | | : : ||:
Db      688 PAGGSGPAGPPGPQGVKGERGSPGGPGAAGFPGGRGPPGPPGSNGNPGPPGSSGAPGKDG 747

Qy      203 LPGDPTSNAT-----SRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGA 245
      || | ||
Db      748 PPGPPGSNGAPGSPGISGPKGDSGPPGERGAPGPQGPAPGPLGIAG-----LTGARGL 802

Qy      246 GGAMCWRRRRRAKP-----SESRHPGP-----GSFGRGGSLLGLGGGGMGMPREAEPE 292
      | | | | | : || | | | | | | : ||
Db      803 AGPPGMPGARGSPGPQGIKENGKPGPSGQNGERGPPGPQGLPGLAGTAGEPGRDGNPGS 862

Qy      293 LGIALRGG-----GAADPPFCPHYEKVSGDYGHPVYIVQDGPP 330
      |: | | | | | | || | ||
Db      863 DGLPGRDGAPGAKGDRGENSGPGAP-----GAPGHP-----GPP 896

```

Search completed: September 15, 2004, 12:40:09
 Job time : 31.761 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2004, 12:39:22 ; Search time 99.5849 Seconds
(without alignments)
1465.220 Million cell updates/sec

Title: US-10-021-121-2
Perfect score: 2450
Sequence: 1 MGPPHSGPGGVRVGALLLLG.....TTLLRQRASVEAEAGQHGPL 455

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1335176 seqs, 320689617 residues

Total number of hits satisfying chosen parameters: 1335176

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query	
No.	Score	Match Length DB ID	Description

1	2450	100.0	455	13	US-10-021-121-2	Sequence 2, Appli
2	1841	75.1	340	13	US-10-021-121-4	Sequence 4, Appli
3	1837	75.0	340	13	US-10-138-787-3	Sequence 3, Appli
4	1835	74.9	340	15	US-10-417-924A-2	Sequence 2, Appli
5	1550	63.3	285	16	US-10-408-765A-2695	Sequence 2695, Ap
6	623	25.4	346	13	US-10-021-121-9	Sequence 9, Appli
7	623	25.4	346	16	US-10-356-289-2	Sequence 2, Appli
8	620.5	25.3	333	9	US-09-754-105-2	Sequence 2, Appli
9	620.5	25.3	333	9	US-09-978-339-2	Sequence 2, Appli
10	620.5	25.3	333	13	US-10-021-121-10	Sequence 10, Appl
11	620.5	25.3	333	15	US-10-331-496A-63	Sequence 63, Appl
12	613.5	25.0	333	13	US-10-138-787-4	Sequence 4, Appli
13	599.5	24.5	345	13	US-10-138-787-5	Sequence 5, Appli
14	489	20.0	89	9	US-09-862-179A-17	Sequence 17, Appl
15	489	20.0	89	13	US-10-138-787-13	Sequence 13, Appl
16	284.5	11.6	92	9	US-09-864-761-48262	Sequence 48262, A
17	196.5	8.0	136	9	US-09-864-761-48257	Sequence 48257, A
18	193.5	7.9	106	9	US-09-925-297-639	Sequence 639, App
19	192	7.8	82	9	US-09-862-179A-15	Sequence 15, Appl
20	192	7.8	82	13	US-10-138-787-11	Sequence 11, Appl
21	191.5	7.8	82	9	US-09-862-179A-16	Sequence 16, Appl
22	191.5	7.8	82	13	US-10-138-787-12	Sequence 12, Appl
23	179	7.3	238	9	US-09-904-954-2	Sequence 2, Appli
24	179	7.3	238	10	US-09-733-756-2	Sequence 2, Appli
25	179	7.3	238	14	US-10-241-220-72	Sequence 72, Appl
26	179	7.3	238	15	US-10-295-027-130	Sequence 130, App
27	176	7.2	209	9	US-09-921-984-2	Sequence 2, Appli
28	174.5	7.1	233	13	US-10-138-787-7	Sequence 7, Appli
29	172.5	7.0	218	9	US-09-925-297-510	Sequence 510, App
30	169.5	6.9	201	9	US-09-904-954-4	Sequence 4, Appli
31	169.5	6.9	225	16	US-10-322-696-135	Sequence 135, App
32	169	6.9	201	13	US-10-138-787-8	Sequence 8, Appli
33	168.5	6.9	209	13	US-10-138-787-6	Sequence 6, Appli
34	167.5	6.8	228	8	US-08-578-684-4	Sequence 4, Appli
35	166	6.8	205	13	US-10-138-787-10	Sequence 10, Appl
36	166	6.8	205	14	US-10-171-311-50	Sequence 50, Appl
37	166	6.8	205	15	US-10-372-683-34	Sequence 34, Appl
38	164.5	6.7	204	12	US-10-147-493-288	Sequence 288, App
39	164.5	6.7	204	12	US-10-145-127-288	Sequence 288, App
40	164.5	6.7	204	12	US-10-160-503-288	Sequence 288, App
41	164.5	6.7	204	12	US-10-143-118-288	Sequence 288, App
42	164.5	6.7	204	12	US-10-144-993-288	Sequence 288, App
43	164.5	6.7	204	12	US-10-158-787-288	Sequence 288, App
44	164.5	6.7	204	12	US-10-140-024-288	Sequence 288, App
45	164.5	6.7	204	12	US-10-140-808-288	Sequence 288, App

ALIGNMENTS

RESULT 1
 US-10-021-121-2
 ; Sequence 2, Application US/10021121
 ; Publication No. US20020142444A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Caras, Ingrid W

```

; TITLE OF INVENTION: A2-1 Neurotrophic Factor
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/021,121
; FILING DATE: 06-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/635,130
; FILING DATE: 19-Mar-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Torchia, PhD., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 455 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-021-121-2

```

```

Query Match          100.0%; Score 2450; DB 13; Length 455;
Best Local Similarity 100.0%; Pred. No. 7.6e-187;
Matches 455; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 MGPPHSGPGGVRVGALLLLGLVGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
      |||
Db      1 MGPPHSGPGGVRVGALLLLGLVGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

QY     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
      |||
Db     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

QY    121 SPNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGA VPRKP 180
      |||
Db    121 SPNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGA VPRKP 180

QY    181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
      |||
Db    181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

QY    241 GVAGAGGAMCWRRRRRAKPSERHPGPGSFGRGGS LGLGGGGMGMPREAE PGELGIALRGG 300

```



```

Db      241  |||||GVAGAGGAMCWRRRRAKPSSESRHPGPSFGRGGSLLGLGGGGMGPREAEPGELGIALRGG 300
QY      301  GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYTSISVLEWPILHTIQLFFMRSK 360
Db      301  |||||GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYYTSISVLEWPILHTIQLFFMRSK 360
QY      361  CSRVTTFLFPVQVITTSTCRMTSFSFSTTLNPSMQACRAQMGEFRIRWCFWGDRLGTALF 420
Db      361  |||||CSRVTTFLFPVQVITTSTCRMTSFSFSTTLNPSMQACRAQMGEFRIRWCFWGDRLGTALF 420
QY      421  VLVLLLLLGRNLNMHQTLLRQRASVEAEAGQHGPL 455
Db      421  |||||VLVLLLLLGRNLNMHQTLLRQRASVEAEAGQHGPL 455

```

RESULT 2

US-10-021-121-4

; Sequence 4, Application US/10021121

; Publication No. US20020142444A1

; GENERAL INFORMATION:

; APPLICANT: Caras, Ingrid W

; TITLE OF INVENTION: A2-1 Neurotrophic Factor

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genentech, Inc.

; STREET: 1 DNA Way

; CITY: South San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: WinPatin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/021,121

; FILING DATE: 06-Dec-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/635,130

; FILING DATE: 19-Mar-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Torchia, PhD., Timothy E.

; REGISTRATION NUMBER: 36,700

; REFERENCE/DOCKET NUMBER: P1001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-8674

; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 340 amino acids

; TYPE: Amino Acid

; TOPOLOGY: Linear

; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-10-021-121-4

Query Match 75.1%; Score 1841; DB 13; Length 340;
Best Local Similarity 100.0%; Pred. No. 1.9e-138;
Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy    121 SPNLWGHEFRSHHDYIIATSDGTREGLESQGVCCLTRGMKVLLRVGQSPRGGAVPRKP 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 SPNLWGHEFRSHHDYIIATSDGTREGLESQGVCCLTRGMKVLLRVGQSPRGGAVPRKP 180

Qy    181 VSEMPMERDRGAHAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 VSEMPMERDRGAHAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

Qy    241 GVAGAGGAMCWRRRRRAKPSERHPGPGSFGRGGSGLGLGGGGMGMPREAEPEGELGIALRGG 300
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GVAGAGGAMCWRRRRRAKPSERHPGPGSFGRGGSGLGLGGGGMGMPREAEPEGELGIALRGG 300

Qy    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
```

RESULT 3

US-10-138-787-3

; Sequence 3, Application US/10138787

; Publication No. US20020172984A1

; GENERAL INFORMATION:

; APPLICANT: Holland, Sacha

; APPLICANT: Mbamalu, Geraldine

; APPLICANT: Pawson, Tony

; TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED

; TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR

; TITLE OF INVENTION: TYROSINE KINASES

; FILE REFERENCE: 11757.23USWO

; CURRENT APPLICATION NUMBER: US/10/138,787

; CURRENT FILING DATE: 2002-05-03

; PRIOR APPLICATION NUMBER: US/09/214,631

; PRIOR FILING DATE: 1999-03-12

; PRIOR APPLICATION NUMBER: PCT/CA97/00473

; PRIOR FILING DATE: 1997-07-04

; PRIOR APPLICATION NUMBER: 60/021,272

; PRIOR FILING DATE: 1996-07-05

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3

; LENGTH: 340

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-138-787-3

Query Match 75.0%; Score 1837; DB 13; Length 340;
Best Local Similarity 99.7%; Pred. No. 4.1e-138;
Matches 337; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```
QY      1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
      |||
Db      1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

QY     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLRLRFTIKFQEY 120
      |||
Db     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLRLRFTIKFQEY 120

QY    121 SPNLWGHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGAVPRKP 180
      |||
Db    121 SPNLWGHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLQVGQSPRGGAVPRKP 180

QY    181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPSPMPAVAGAAGGLALLLL 240
      |||
Db    181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPSPMPAVAGAAGGLALLLL 240

QY    241 GVAGAGGAMCWRRRRRAKPSESRRHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGG 300
      |||
Db    241 GVAGAGGAMCWRRRRRAKPSESRRHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGG 300

QY    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
      |||
Db    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
```

RESULT 4

US-10-417-924A-2

; Sequence 2, Application US/10417924A

; Publication No. US20030215918A1

; GENERAL INFORMATION:

; APPLICANT: Samuel Davis, et al.

; TITLE OF INVENTION: BIOLOGICALLY ACTIVE EPH FAMILY LIGANDS

; FILE REFERENCE: REG-341Z

; CURRENT APPLICATION NUMBER: US/10/417,924A

; CURRENT FILING DATE: 2003-04-17

; PRIOR APPLICATION NUMBER: 09/051,994

; PRIOR FILING DATE: 1998-04-24

; PRIOR APPLICATION NUMBER: PCT/US96/17201

; PRIOR FILING DATE: 1996-10-25

; PRIOR APPLICATION NUMBER: 60/007,015

; PRIOR FILING DATE: 1995-10-25

; NUMBER OF SEQ ID NOS: 3

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 340

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: Misc. feature

; LOCATION: (166)

; OTHER INFORMATION: Xaa = unknown or other

US-10-417-924A-2

Query Match 74.9%; Score 1835; DB 15; Length 340;
 Best Local Similarity 99.7%; Pred. No. 5.9e-138;
 Matches 337; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

QY      1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
        |||
Db      1 MGPPHSGPGGVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

QY     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRDLRFTIKFQEY 120
        |||
Db     61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRDLRFTIKFQEY 120

QY    121 SPNLWGHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGA VPRKP 180
        |||
Db    121 SPNLWGHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGA VPRKP 180

QY    181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
        |||
Db    181 VSEMPMERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240

QY    241 GVAGAGGAMCWRRRRRAKPSES RHPGPSFGRGGS LGLGGGGMGPREAEPGELGIALRGG 300
        |||
Db    241 GVAGAGGAMCWRRRRRAKPSES RHPGPSFGRGGS LGLGGGGMGPREAEPGELGIALRGG 300

QY    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
        |||
Db    301 GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY 338

```

RESULT 5

US-10-408-765A-2695

; Sequence 2695, Application US/10408765A

; Publication No. US20040101874A1

; GENERAL INFORMATION:

; APPLICANT: Ghosh, Soumitra S.

; APPLICANT: Fahy, Eoin D.

; APPLICANT: Zhang, Bing

; APPLICANT: Gibson, Bradford W.

; APPLICANT: Taylor, Steven W.

; APPLICANT: Glenn, Gary M.

; APPLICANT: Warnock, Dale E.

; TITLE OF INVENTION: TARGETS FOR THERAPEUTIC INTERVENTION

; TITLE OF INVENTION: IDENTIFIED IN THE MITOCHONDRIAL PROTEOME

; FILE REFERENCE: 660088.465

; CURRENT APPLICATION NUMBER: US/10/408,765A

; CURRENT FILING DATE: 2003-04-04

; NUMBER OF SEQ ID NOS: 3077

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 2695

; LENGTH: 285

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-408-765A-2695

Query Match 63.3%; Score 1550; DB 16; Length 285;
 Best Local Similarity 100.0%; Pred. No. 2.5e-115;

Matches 283; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      56 DRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRDLDLRFTI 115
      |||||||
Db      1 DRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRDLDLRFTI 60

Qy     116 KFQEYSPNLWGHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGA 175
      |||||||
Db      61 KFQEYSPNLWGHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGA 120

Qy     176 VPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTS NATSRGAEGPLPPPSMPAVAGAAGGL 235
      |||||||
Db     121 VPRKPVSEMPMERDRGAAHSLEPGKENLPGDPTS NATSRGAEGPLPPPSMPAVAGAAGGL 180

Qy     236 ALLLLGVAGAGGAMCWRRRRAKPSERHPGPGSFGRGSLGLGGGGMGPREAEPGELGI 295
      |||||||
Db     181 ALLLLGVAGAGGAMCWRRRRAKPSERHPGPGSFGRGSLGLGGGGMGPREAEPGELGI 240

Qy     296 ALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPNIIY 338
      |||||||
Db     241 ALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPNIIY 283
```

RESULT 6

US-10-021-121-9

; Sequence 9, Application US/10021121

; Publication No. US20020142444A1

; GENERAL INFORMATION:

; APPLICANT: Caras, Ingrid W
; TITLE OF INVENTION: A2-1 Neurotrophic Factor
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

; COMPUTER READABLE FORM:

; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatin (Genentech)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/021,121
; FILING DATE: 06-Dec-2001
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/635,130
; FILING DATE: 19-Mar-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Torchia, PhD., Timothy E.
; REGISTRATION NUMBER: 36,700
; REFERENCE/DOCKET NUMBER: P1001

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 650/225-8674
; TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 9:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 346 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
 US-10-021-121-9

Query Match 25.4%; Score 623; DB 13; Length 346;
 Best Local Similarity 39.2%; Pred. No. 2.7e-41;
 Matches 143; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

```

QY      8 PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
      ||  :| |: |: : |      :||| |:| |:| : | |:|:|:|:|:|:
Db      4 PGQRWLGKWLVMVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

QY     62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRCEAPPAPNLLLTCDRPLDLRFTIKFQEYS 121
      ||| | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     64 CPRAEAGRP-----Y EYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

QY    122 PNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
      || | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    119 PNYMGLEFKKHHDYITSTSNGLSLEGLNREGGVCRTMTMKIIMKVGQDPNAVTPQEQLTT 178

QY    182 SEMPMERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
      | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    179 SRPSKEADNTVKMATQAPGSRGSLGSDSGKHETV NQEEKSGP-----GASGGSSGDPD 231

QY    237 -----LLLLGVAGAGGA-----MCWRRRRRAKPSERHPGPGSFRGGSLGL 277
      : | | | | | | | | | | | | | | | | | | | | | | | | |
Db    232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLLKLRKRHRKHTQQ-----RAAALSL 282

QY    278 ----GGGGMGMPREAEPEGELGIALRGGAADPPFCPHYEKVSGDYGHVPVYIVQDGPPQSP 333
      || | | | | | | | | | | | | | | | | | | | | | | | | |
Db    283 STLASPKGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHVPVYIVQEMPPQSP 339

QY    334 PNIYY 338
      ||| |
Db    340 ANIYY 344
  
```

RESULT 7

US-10-356-289-2

; Sequence 2, Application US/10356289

; Publication No. US20040022767A1

; GENERAL INFORMATION:

; APPLICANT: Lyman, Stewart D.

; APPLICANT: Beckmann, M. Patricia

; APPLICANT: Baum, Peter R.

; APPLICANT: Carpenter, Melissa K.

; TITLE OF INVENTION: NOVEL CYTOKINE DESIGNATED ELK LIGAND

; FILE REFERENCE: GENENT.67CPDV3

; CURRENT APPLICATION NUMBER: US/10/356,289

; CURRENT FILING DATE: 2003-01-31

; PRIOR APPLICATION NUMBER: US/09/039,642B

; PRIOR FILING DATE: 1998-03-16

; PRIOR APPLICATION NUMBER: 08/213,403

```
; PRIOR FILING DATE: 1994-03-15
; PRIOR APPLICATION NUMBER: 07/977,693
; PRIOR FILING DATE: 1992-11-13
; PRIOR APPLICATION NUMBER: 08/747,240
; PRIOR FILING DATE: 1996-10-12
; PRIOR APPLICATION NUMBER: 08/460,741
; PRIOR FILING DATE: 1995-06-02
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 346
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-356-289-2
```

```
Query Match          25.4%; Score 623; DB 16; Length 346;
Best Local Similarity 39.2%; Pred. No. 2.7e-41;
Matches 143; Conservative 48; Mismatches 116; Indels 58; Gaps 9;
```

```
Qy      8 PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRDL 61
      || :| |: |: : | :||| |:| |:| :| |:|:|:|:|:|:|
Db      4 PGQRWLKGWLVMVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy     62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRCEAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
      ||| | | :||| | | | | :|:|:|:|:|:|:|:|:|
Db     64 CPRAEAGRP-----YEYYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118

Qy    122 PNLWGHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGA VPRKPV 181
      || | |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db    119 PNYMGLEFKKHHDYITSTSNGLSLEGLNREGGVCRTTRTMKIIMKVGQDPNAVTPQLTT 178

Qy    182 SEMPMERDRGAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
      | | | : : || | | : | | | | :|:|:|
Db    179 SRPSKEADNTVKMATQAPGSRGSLGDSGDKHETVNQEEKSGP-----GASGGSSGDPD 231

Qy    237 -----LLLLGVAGAGGA-----MCWRRRRRAKPSES RHPGPGSFGRGGSLGL 277
      : | || | : |:| | : | :| |
Db    232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLKLKRHRKHTQQ-----RAAALSL 282

Qy    278 ----GGGGMGPREAEPGELGIALRGGAADPPFCPHYEKVSGDYGHVPVYIVQDGPPQSP 333
      || | || : : | | : :|:|:|:|:|:|:|:|:|:|
Db    283 STLASPKGGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHVPVYIVQEMPQSP 339

Qy    334 PNIYY 338
      |||
Db    340 ANIYY 344
```

RESULT 8

US-09-754-105-2

```
; Sequence 2, Application US/09754105
; Patent No. US20010009768A1
; GENERAL INFORMATION:
; APPLICANT: Cerretti, Douglas
; APPLICANT: Reddy, Pranhitha
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING CYTOKINE DESIGNATED LERK-5
; FILE REFERENCE: 28232
```

; CURRENT APPLICATION NUMBER: US/09/754,105
; CURRENT FILING DATE: 2001-01-03
; PRIOR APPLICATION NUMBER: 09/329,531
; PRIOR FILING DATE: 1999-06-10
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 333
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-754-105-2

Query Match 25.3%; Score 620.5; DB 9; Length 333;
Best Local Similarity 40.5%; Pred. No. 4.1e-41;
Matches 133; Conservative 52; Mismatches 130; Indels 13; Gaps 5;

Qy	14	GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS	73
		:: : : : : : : :: : :	
Db	14	GVLMLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV--DSKTV	70
Qy	74	PNYEFYKLYLVGGAQGRRCAPPAPNLLLTCDRDLRFTIKFQEYSPNLWGHEFRSHH	133
		:: : : : :: : : :	
Db	71	GQY EYKVMVDKQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK	130
Qy	134	DYYIIATSDGTREGLESLOGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR	190
		: : : ::: : : : : : :	
Db	131	DYYIISTSNGLSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN	190
Qy	191	GAHSLEPGKENLPGDPTSNAATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC	250
		: : : : : : : : : : : :	
Db	191	GRSSTTSFVKPNPGSSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL	250
Qy	251	WRRRRRAKPSESRHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPH	310
		: : : : : :	
Db	251	KYRRRHRKHSPQHTTTLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVFCPH	303
Qy	311	YEKVS GDYGHVPYIVQDGP PQSPPNIIY	338
		:	
Db	304	YEKVS GDYGHVPYIVQEMPPQSPANIYY	331

RESULT 9

US-09-978-339-2

; Sequence 2, Application US/09978339

; Patent No. US20020103358A1

; GENERAL INFORMATION:

; APPLICANT: Cerretti, Douglas P.

; Reddy, Pranhitha

; TITLE OF INVENTION: No. US20020103358A1el Cytokine Designated Lerk-5

; NUMBER OF SEQUENCES: 3

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Immunex Corporation

; STREET: 51 University Street

; CITY: Seattle

; STATE: Washington

; COUNTRY: US

; ZIP: 98101


```

;      COMPUTER READABLE FORM:
;      MEDIUM TYPE: Floppy disk
;      COMPUTER: Apple Macintosh
;      OPERATING SYSTEM: Apple 7.1
;      SOFTWARE: Microsoft Word, Version 5.1a
;
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/09/978,339
;      FILING DATE: 15-Oct-2001
;      CLASSIFICATION: <Unknown>
;
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 08/271,948
;      FILING DATE: <Unknown>
;
;      ATTORNEY/AGENT INFORMATION:
;      NAME: Seese, Kathryn A.
;      REGISTRATION NUMBER: 32,172
;      REFERENCE/DOCKET NUMBER: 2823
;
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: (206) 587-0430
;      TELEFAX: (206) 233-0644
;      TELEX: 756822
;
;      INFORMATION FOR SEQ ID NO: 2:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 333 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
;      MOLECULE TYPE: protein
;      SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-978-339-2

```

```

Query Match          25.3%;  Score 620.5;  DB 9;  Length 333;
Best Local Similarity 40.5%;  Pred. No. 4.1e-41;
Matches 133;  Conservative 52;  Mismatches 130;  Indels 13;  Gaps 5;

```

```

Qy      14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
      | |::| : : |||:||||:| :| | |||||:|::|: :
Db      14 GVLMVLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70

Qy      74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLRLRFTIKFQEYSPNLWGHEFRSHH 133
      ||::|:| | || || | :|| |::| |||||:|||| | | :
Db      71 GQYEYYKVYMDKQADRCTIKKENTPLLNCAPDQDIKFTIKFQEFSPNLWGLEFQKNK 130

Qy     134 DYYIIATSDGTREGLESLOGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
      ||||:|:|: |||: :||| || ||:|:| || | | : | :|
Db     131 DYYIISTSNGLSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190

Qy     191 GAAHSLEPGKENLPGDPTSNAATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
      | : : | : || | : : : : : | | | : : : :
Db     191 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL 250

Qy     251 WRRRRRAKPSESRHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGGAADPPFCPH 310
      ||| : :| | : : | :|| : : | | || |||
Db     251 KYRRRHRKHSPQHTTTLSTLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVFCPH 303

Qy     311 YEKVSGDYGHPVYIVQDGPQSPNIIY 338
      |||||:|||||: |||| |||
Db     304 YEKVSGDYGHPVYIVQEMPQSPANIY 331

```

RESULT 10
 US-10-021-121-10
 ; Sequence 10, Application US/10021121
 ; Publication No. US20020142444A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Caras, Ingrid W
 ; TITLE OF INVENTION: A2-1 Neurotrophic Factor
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Genentech, Inc.
 ; STREET: 1 DNA Way
 ; CITY: South San Francisco
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 94080
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: WinPatin (Genentech)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/021,121
 ; FILING DATE: 06-Dec-2001
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/635,130
 ; FILING DATE: 19-Mar-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Torchia, PhD., Timothy E.
 ; REGISTRATION NUMBER: 36,700
 ; REFERENCE/DOCKET NUMBER: P1001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650/225-8674
 ; TELEFAX: 650/952-9881
 ; INFORMATION FOR SEQ ID NO: 10:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 333 amino acids
 ; TYPE: Amino Acid
 ; TOPOLOGY: Linear
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
 US-10-021-121-10

Query Match 25.3%; Score 620.5; DB 13; Length 333;
 Best Local Similarity 40.5%; Pred. No. 4.1e-41;
 Matches 133; Conservative 52; Mismatches 130; Indels 13; Gaps 5;

Qy 14 GALLLLGVLGLVSGLSLEPVYWNSSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
 | |::| : : |||:||||:| :| | |||||::|:::| :
 Db 14 GVLMVLCRTAISKSIIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70
 Qy 74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRDLRLFTIKFQEYSPNLWGHEFRSHH 133
 ||::|::| | || || | :|| :::| |||||::| ||||| ||: :
 Db 71 GQYEYYKVYMVMDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130
 Qy 134 DYYIIATSDGTREGLESLOGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
 |||||::|::| |||:: :||| || |||:::| | | : | :|

Db 131 DYYIISTSNGLSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190
 Qy 191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
 | : : | : || | :: : : : || | | : :: : :
 Db 191 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL 250
 Qy 251 WRRRRRAKPSESRRHPGPGSFGRRGSLGLGGGGMGPREAEPGELGIALRGGAADPPFCPH 310
 ||| : :| | : | : || :: | || || ||
 Db 251 KYRRRRHRKHSPQHTTTLSTLSTLATPKRSGNN----NGSEPSDIIPLR---TADSVFCPH 303
 Qy 311 YEKVSGDYGHPVYIVQDGPQPSPNNIYY 338
 ||||| ||||| ||||| : |||| ||||
 Db 304 YEKVSGDYGHPVYIVQEMPQPSPANNIYY 331

RESULT 11

US-10-331-496A-63

; Sequence 63, Application US/10331496A

; Publication No. US20030228305A1

; GENERAL INFORMATION:

; APPLICANT: FRANTZ, GRETCHEN

; APPLICANT: HILLAN, KENNETH J.

; APPLICANT: PHILLIPS, HEIDI S.

; APPLICANT: POLAKIS, PAUL

; APPLICANT: SMITH, VICTORIA

; APPLICANT: SPENCER, SUSAN D.

; APPLICANT: WILLIAMS, P. MICKEY

; APPLICANT: WU, THOMAS D.

; APPLICANT: ZHANG, ZEMIN

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND

; TITLE OF INVENTION: TREATMENT OF TUMOR

; FILE REFERENCE: P5014R1-PCT

; CURRENT APPLICATION NUMBER: US/10/331,496A

; CURRENT FILING DATE: 2002-12-30

; PRIOR APPLICATION NUMBER: US 60/345,444

; PRIOR FILING DATE: 2002-01-02

; PRIOR APPLICATION NUMBER: US 60/351,885

; PRIOR FILING DATE: 2002-01-25

; PRIOR APPLICATION NUMBER: US 60/360,066

; PRIOR FILING DATE: 2002-02-25

; PRIOR APPLICATION NUMBER: US 60/362,004

; PRIOR FILING DATE: 2002-03-05

; PRIOR APPLICATION NUMBER: US 60/366,869

; PRIOR FILING DATE: 2002-03-20

; PRIOR APPLICATION NUMBER: US 60/366,284

; PRIOR FILING DATE: 2002-03-21

; PRIOR APPLICATION NUMBER: US 60/368,679

; PRIOR FILING DATE: 2002-03-28

; PRIOR APPLICATION NUMBER: US 60/404,809

; PRIOR FILING DATE: 2002-08-19

; PRIOR APPLICATION NUMBER: US 60/405,645

; PRIOR FILING DATE: 2002-08-21

; NUMBER OF SEQ ID NOS: 95

; SEQ ID NO 63

; LENGTH: 333

; TYPE: PRT

; ORGANISM: Homo sapien

US-10-331-496A-63

Query Match 25.3%; Score 620.5; DB 15; Length 333;
Best Local Similarity 40.5%; Pred. No. 4.1e-41;
Matches 133; Conservative 52; Mismatches 130; Indels 13; Gaps 5;

```
Qy      14 GALLLLGVLGLVSGLSLEPVYWSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
      | |::| : : |||:||||:| :| | |||||:|::|: : :
Db      14 GVLMLVCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70

Qy      74 PNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRPDLRLFTIKFQEYSPNLWGHEFRSHH 133
      ||::|:|:| | || || | :|| |::| |||||:||||| ||: :
Db      71 GQYEEYKVMVDKDQADRCTIKKENTPLLNCAKPDQDIKFTIKFQEFSPNLWGLEFQKNK 130

Qy     134 DYYIIATSDGTREGLESIQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
      |||||:|:|:| |||:: :||| || |::|:| | | : | :|
Db     131 DYYIIISTSNGLSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190

Qy     191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
      | : : | : || | : : : : : || | | : : : : :
Db     191 GRSSTTSPFVKPNPGSSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL 250

Qy     251 WRRRRRAKPSESRHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
      ||| : :| | : | : || : : | || || |||
Db     251 KYRRRRHRKHSPQHTTTLSTLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVFCPH 303

Qy     311 YEKVSGDYGHPVYIVQDGPPQSPPNIIY 338
      ||||| ||||| ||||| : |||| ||||
Db     304 YEKVSGDYGHPVYIVQEMPPQSPANIYY 331
```

RESULT 12

US-10-138-787-4

```
; Sequence 4, Application US/10138787
; Publication No. US20020172984A1
; GENERAL INFORMATION:
; APPLICANT: Holland, Sacha
; APPLICANT: Mbamalu, Geraldine
; APPLICANT: Pawson, Tony
; TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
; TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
; TITLE OF INVENTION: TYROSINE KINASES
; FILE REFERENCE: 11757.23USWO
; CURRENT APPLICATION NUMBER: US/10/138,787
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/09/214,631
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: PCT/CA97/00473
; PRIOR FILING DATE: 1997-07-04
; PRIOR APPLICATION NUMBER: 60/021,272
; PRIOR FILING DATE: 1996-07-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 333
; TYPE: PRT
; ORGANISM: Homo sapiens
```

US-10-138-787-4

Query Match 25.0%; Score 613.5; DB 13; Length 333;
Best Local Similarity 40.5%; Pred. No. 1.5e-40;
Matches 133; Conservative 54; Mismatches 128; Indels 13; Gaps 6;

Qy 14 GALLLLGVLGLVSGLSLEPVYWSANKRFQAEAGGYVLYPQIGDRDLLCPRARPPGPHSS 73
| |::| : : |||:| ||:| :| | |||||::|::|::| :
Db 14 GVLMLCRTAISKSIVLEPIYMSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70

Qy 74 PNYEFYKLYLVGGAQGRRCAPPAPNLLLLTCDRPDLRLFTIKFQEYSPNLWGHEFRSHH 133
||:|::|:| | || || | :|| |::| |||||::| ||||| ||: :
Db 71 GQYEYKVMVDKQADRCTIKKENTPLLNCAPDQDIKFTIKFQEFSPNLWGLEFQKNK 130

Qy 134 DYYIIATSDGTREGLESIQGGVCLTRGMKVLLRVGQ-SPRGGAVPRKPVSEMP-MER-DR 190
||||:|::|:| |||:: :||| || ||:|::| | : | : | : | :
Db 131 DYYIISTSNGLSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTPNKDPTRRPELEAGTN 190

Qy 191 GAAHSLEPGKENLPGDPTSNAISRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
| : : | : || | : : : : : || | | : : : : :
Db 191 GRSSTTSPFVKPNPGSSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL 250

Qy 251 WRRRRRAKPSESRRHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
||| : :| | : | : || : : | || || |||
Db 251 KYRRRRHRKHSPQHTTTLSTLATPKRSGNN----NGSEPSDIIIPLR---TADSVFCPH 303

Qy 311 YEKVS GDYGHVPVYIVQDGPQSPNIIYY 338
||||||| |||||: ||||| ||||
Db 304 YEKVS GDYGHVPVYIVQEMPPQSPANIIYY 331

RESULT 13

US-10-138-787-5

; Sequence 5, Application US/10138787
; Publication No. US20020172984A1
; GENERAL INFORMATION:
; APPLICANT: Holland, Sacha
; APPLICANT: Mbamalu, Geraldine
; APPLICANT: Pawson, Tony
; TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED
; TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR
; TITLE OF INVENTION: TYROSINE KINASES
; FILE REFERENCE: 11757.23USWO
; CURRENT APPLICATION NUMBER: US/10/138,787
; CURRENT FILING DATE: 2002-05-03
; PRIOR APPLICATION NUMBER: US/09/214,631
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: PCT/CA97/00473
; PRIOR FILING DATE: 1997-07-04
; PRIOR APPLICATION NUMBER: 60/021,272
; PRIOR FILING DATE: 1996-07-05
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-138-787-5

```
Query Match          24.5%;  Score 599.5;  DB 13;  Length 345;
Best Local Similarity 38.4%;  Pred. No. 2e-39;
Matches 140;  Conservative 50;  Mismatches 116;  Indels 59;  Gaps 10;

Qy      8 PGGVRVG----ALLLLGVLGLVSGL--SLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLL 61
      ||| :|      |:::  :  | : |  :||| | :| | :| :  | |::|::|::|::|
Db      4 PGGRWLKGWLYAMVVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63

Qy     62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRC EAPPAPNLLLTCDRPDLDLRFTIKFQEYS 121
      || |  |      ||:|||||  |  |  |  :|:|:|:|:  :|:|:|:|:|:|
Db     64 CPPAEAGRP-----YEYYKLYLVRPEQAAACSTVLDPMVLVTCNRPEQEIRFTIKFQEFS 118

Qy    122 PNLWGHEFRSHHDYIIATSDGTREGLESIQGGVCLTRGMKVLLRVGQSPRGGA VPRKPV 181
      ||  | ||: |||||  :|:|:  |||:  :|||  ||  ||:::|  |  :
Db    119 PNYMGLEFKKHHDYITSTSNGLSLEGLNREGGVCRTRTMKIIMKVGQDPNAVTP EQLT 178

Qy    182 SEMP MERDRGAAHSLE-PGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
      |  |  |  : : ||  ||  :  |  |  ||:|  :
Db    179 SRPSKEADNTVKMATQAPGSRGSLGSDSGKHETV NQEEKSGP-----GASGGSSGDPD 231

Qy    237 -----LLLLGVAGAGGA-----MCWRRRRRAKPSES RHPGPGSFGRGGS LGL 277
      : |  |||  :  :|  | :  | :|  |
Db    232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLLLKLPKRHRKHTQ-----RAAALSL 281

Qy    278 ----GGGGMGPREAEPGELGIALRGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
      || |  || : : |  :  : |||||:|:|:|:|:|:|:|:|:|:|:|
Db    282 STIASPKGGSGTAGTEPSDIIPL---FTTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 338

Qy    334 PNIYY 338
      ||||
Db    339 ANIYY 343
```

RESULT 14

US-09-862-179A-17

; Sequence 17, Application US/09862179A

; Patent No. US20020147306A1

; GENERAL INFORMATION:

; APPLICANT: Lin, Danny

; APPLICANT: Pawson, Anthony

; TITLE OF INVENTION: PEPTIDES THAT MODULATE THE INTERACTION OF B CLASS EPHRINS

; TITLE OF INVENTION: AND PDZ DOMAINS

; FILE REFERENCE: MTSI-P01-009

; CURRENT APPLICATION NUMBER: US/09/862,179A

; CURRENT FILING DATE: 2001-05-21

; NUMBER OF SEQ ID NOS: 44

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 17

; LENGTH: 89

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-862-179A-17

```
Query Match          20.0%;  Score 489;  DB 9;  Length 89;
Best Local Similarity 100.0%;  Pred. No. 2.4e-31;
```

Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 252 RRRRAKPSES RHPGPGSFGRGSSLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPHY 311
 |||
 Db 1 RRRRAKPSES RHPGPGSFGRGSSLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPHY 60

Qy 312 EKVSGDYGHPVYIVQDGPPQSPPNIYY 338
 |||
 Db 61 EKVSGDYGHPVYIVQDGPPQSPPNIYY 87

RESULT 15

US-10-138-787-13

; Sequence 13, Application US/10138787

; Publication No. US20020172984A1

; GENERAL INFORMATION:

; APPLICANT: Holland, Sacha

; APPLICANT: Mbamalu, Geraldine

; APPLICANT: Pawson, Tony

; TITLE OF INVENTION: OLIGOMERIZED RECEPTORS WHICH AFFECT PATHWAYS REGULATED

; TITLE OF INVENTION: BY TRANSMEMBRANE LIGANDS FOR ELK-RELATED RECEPTOR

; TITLE OF INVENTION: TYROSINE KINASES

; FILE REFERENCE: 11757.23USWO

; CURRENT APPLICATION NUMBER: US/10/138,787

; CURRENT FILING DATE: 2002-05-03

; PRIOR APPLICATION NUMBER: US/09/214,631

; PRIOR FILING DATE: 1999-03-12

; PRIOR APPLICATION NUMBER: PCT/CA97/00473

; PRIOR FILING DATE: 1997-07-04

; PRIOR APPLICATION NUMBER: 60/021,272

; PRIOR FILING DATE: 1996-07-05

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 13

; LENGTH: 89

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-138-787-13

Query Match 20.0%; Score 489; DB 13; Length 89;

Best Local Similarity 100.0%; Pred. No. 2.4e-31;

Matches 87; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 252 RRRRAKPSES RHPGPGSFGRGSSLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPHY 311
 |||
 Db 1 RRRRAKPSES RHPGPGSFGRGSSLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPHY 60

Qy 312 EKVSGDYGHPVYIVQDGPPQSPPNIYY 338
 |||
 Db 61 EKVSGDYGHPVYIVQDGPPQSPPNIYY 87

Search completed: September 15, 2004, 12:55:53

Job time : 101.585 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 15, 2004, 12:29:25 ; Search time 88.1384 Seconds
(without alignments)
1628.811 Million cell updates/sec

Title: US-10-021-121-2
Perfect score: 2450
Sequence: 1 MGPPHSGPGGVRVGALLLG.....TTLRQRASVEAEAGQHGPL 455

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

%
Result Query
No. Score Match Length DB ID Description

1	914	37.3	331	13	Q90Z31	Q90z31 brachydanio
2	910	37.1	327	13	Q9PT69	Q9pt69 xenopus lae
3	620.5	25.3	333	13	Q9PUJ4	Q9puj4 gallus gall
4	607	24.8	341	13	Q90Z33	Q90z33 brachydanio
5	596.5	24.3	334	13	Q90Z32	Q90z32 brachydanio
6	331	13.5	205	13	Q9W6H9	Q9w6h9 xenopus lae
7	214.5	8.8	237	5	Q9U3M2	Q9u3m2 caenorhabdi
8	198.5	8.1	279	5	Q9U474	Q9u474 caenorhabdi
9	192	7.8	652	5	Q9V4E1	Q9v4e1 drosophila
10	178.5	7.3	202	13	Q98TZ1	Q98tz1 gallus gall
11	168.5	6.9	205	4	Q8N578	Q8n578 homo sapien
12	167	6.8	205	11	Q9D7K8	Q9d7k8 mus musculu
13	163.5	6.7	206	11	Q9CZS8	Q9czs8 mus musculu
14	155.5	6.3	675	6	Q9N178	Q9n178 sus scrofa
15	155	6.3	229	13	O93431	O93431 brachydanio
16	153.5	6.3	217	13	Q7SY61	Q7sy61 xenopus lae
17	153.5	6.3	1691	11	Q9ESQ2	Q9esq2 mus musculu
18	151.5	6.2	1447	13	Q9IB91	Q9ib91 xenopus lae
19	150	6.1	2936	6	Q7YRK8	Q7yrk8 canis famil
20	149	6.1	325	5	O17036	O17036 caenorhabdi
21	149	6.1	569	5	Q17208	Q17208 bombyx mori
22	148.5	6.1	316	5	Q19111	Q19111 caenorhabdi
23	147	6.0	921	11	Q8BSQ4	Q8bsq4 mus musculu
24	146.5	6.0	590	5	Q86BH0	Q86bh0 drosophila
25	146.5	6.0	778	5	Q86BH1	Q86bh1 drosophila
26	146.5	6.0	792	5	Q8MT89	Q8mt89 drosophila
27	146.5	6.0	888	11	Q8CCZ8	Q8ccz8 mus musculu
28	146.5	6.0	1140	11	Q61434	Q61434 mus musculu
29	146.5	6.0	1449	13	Q802B5	Q802b5 xenopus lae
30	146.5	6.0	1491	13	Q91718	Q91718 xenopus lae
31	146.5	6.0	1491	13	Q7ZTM4	Q7ztm4 xenopus lae
32	146	6.0	675	13	Q90800	Q90800 gallus gall
33	146	6.0	1669	11	Q9QZS0	Q9qzs0 mus musculu
34	145.5	5.9	305	5	O17805	O17805 caenorhabdi
35	145.5	5.9	308	5	Q94620	Q94620 meloidogyne
36	145	5.9	680	11	Q9D0D2	Q9d0d2 mus musculu
37	144.5	5.9	309	5	Q25466	Q25466 meloidogyne
38	144.5	5.9	1269	13	Q7T2Z7	Q7t2z7 gallus gall
39	144.5	5.9	1347	4	Q96QB3	Q96qb3 homo sapien
40	144.5	5.9	1420	13	Q90W37	Q90w37 gallus gall
41	143.5	5.9	775	16	Q9F342	Q9f342 streptomyce
42	143	5.8	445	5	Q8MZ49	Q8mz49 drosophila
43	143	5.8	1684	6	Q8HYC1	Q8hyc1 canis famil
44	143	5.8	1688	6	Q866Z2	Q866z2 canis famil
45	143	5.8	1747	5	Q26640	Q26640 strongyloce

ALIGNMENTS

RESULT 1

Q90Z31

ID Q90Z31 PRELIMINARY; PRT; 331 AA.
AC Q90Z31;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Ephrin B3.
GN EFNB3.
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21290827; PubMed=11397014;
RA Chan J., Mably J.D., Serluca F.C., Chen J.N., Goldstein N.B.,
RA Thomas M.C., Cleary J.A., Brennan C., Fishman M.C., Roberts T.M.;
RT "Morphogenesis of prechordal plate and notochord requires intact
RT eph/ephrin b signaling."
RL Dev. Biol. 234:470-482(2001).
DR EMBL; AF375227; AAK64277.1; -.
DR ZFIN; ZDB-GENE-010618-3; efnb3.
DR GO; GO:0016020; C:membrane; IEA.
DR InterPro; IPR008972; Cupredoxin.
DR InterPro; IPR001799; Ephrin.
DR Pfam; PF00812; Ephrin; 1.
DR PRINTS; PR01347; EPHRIN.
DR ProDom; PD002533; Ephrin; 1.
DR PROSITE; PS01299; EPHRIN; 1.
SQ SEQUENCE 331 AA; 35638 MW; 6A5EACD509A09818 CRC64;

Query Match 37.3%; Score 914; DB 13; Length 331;
Best Local Similarity 54.5%; Pred. No. 1.3e-64;
Matches 188; Conservative 43; Mismatches 74; Indels 40; Gaps 10;

Qy	10	GVRVGALLLLGVLGLVSGLSLEPVYWNSANKRFQAEAGGYVLYPQIGDRLDLLCPRARPPG	69
		: : : : : : : : :	
Db	9	GLGILLIFLVDLLG-ITATNMEPIYWNSLNKRFSDDKGYVLYPQIGDRLDLICPSSDPPG	67
Qy	70	PHSSPNYEFYKLYLVGG-AQGRRCCEAPPAPNLLLTCDRDLRFTIKFQEYSPNLWGHE	128
		: : :	
Db	68	PRAPADYEYYKLYLVSSREQADRCEVTGAPNLLLTCDKPNSDMRFTIKFQEYSPNLWGHE	127
Qy	129	FRSHHDYIIATSDGTREGLESLOGGVCLTRGMKVLLRVGQSPRG-GAVPRKPVSEMPME	187
		: : :	
Db	128	FKTNHDYFIIATSDGTRQGLES MRGGVCATQGMKVVLKVGQSPYGLPAKSPKPDS-----	182
Qy	188	RDRGAHSLLEPGKENLPGDPTSNAT-----SRGAEGPLPPPSMPAVAGAAGGLALLL	239
		:	
Db	183	-----AGRINNPNGTGNSTHPQIPPRGSGGENGPLPASNIAVIAGAAGGSAFLL	232
Qy	240	LGVAGAGGAMCWRRRRAKPSERHPGPGSFG-----RGGSLGLGGGGMGPREAEPGEL	293
		:	
Db	233	L-VTAVICVVCYRRRHAKHSESHHP-PLSLSSLTSPKRGCGGGVGGGNNNG---SEPSDI	287
Qy	294	GIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIIY	338
		: :	
Db	288	IIPLR---TSDSAYCPHYEKVSGDYGHPVYIVQEMPQSPANIY	329

RESULT 2
Q9PT69

ID Q9PT69 PRELIMINARY; PRT; 327 AA.
AC Q9PT69;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Ephrin-B3 precursor.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=20099673; PubMed=10633856;
RA Helbling P.M., Saulnier D.M.E., Robinson V., Christiansen J.H.,
RA Wilkinson D.G., Brandli A.W.;
RT "Comparative analysis of embryonic gene expression defines potential
RT interaction sites for Xenopus EphB4 receptors with ephrin-B ligands.";
RL Dev. Dyn. 216:361-373(1999).
DR EMBL; AJ236866; CAB65511.1; -.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR002086; Aldehyde_dehydr.
DR InterPro; IPR008972; Cupredoxin.
DR InterPro; IPR001799; Ephrin.
DR Pfam; PF00812; Ephrin; 1.
DR PRINTS; PR01347; EPHRIN.
DR ProDom; PD002533; Ephrin; 1.
DR PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
DR PROSITE; PS01299; EPHRIN; 1.
KW Signal.
FT SIGNAL 1 24 POTENTIAL.
SQ SEQUENCE 327 AA; 35913 MW; 4BB0FA39D4C22DCD CRC64;

Query Match 37.1%; Score 910; DB 13; Length 327;
Best Local Similarity 60.1%; Pred. No. 2.6e-64;
Matches 190; Conservative 30; Mismatches 82; Indels 14; Gaps 8;

Qy 25 VSGLSLEPVYWNSSANKRFQAEAGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLV 84
:| |||:|:||||:||||: ||||| ||||| |||||: | || | ||:|||||
Db 22 ISALSLDPIYWNSSNKRFEDETEGYVLYPQIGDRLDLLCPRSEPQGPFSPPYEEYKLYLV 81
Qy 85 GGAQG-RRCEAPPAPNLLLTCDRPDLDLRFITKFQEYSPNLWGHEFRSHHDYIIATSDG 143
| : | ||||| ||||| |||||:|||||:| |||||
Db 82 GTKEEMSSCSILRTPNLLLTCDRPSQDLRFITKFQEFSPNLWGHEFQSQRDYIIATSDG 141
Qy 144 TREGLESQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAHSL-EPGKEN 202
| :|:|:||||| |:|||| |:|||| | ||:| | :| | :| :|
Db 142 TMDGIETLQGGVCETKGMKVTLKVGQSPNGATPPRRPSS---AGKDSGISPSVPNPDPIN 198
Qy 203 LPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMCWRRRRAKPSER 262
: |: : ||| | |||| :| ||||| ||||| | | :| ||:| | :|
Db 199 V-GETSGNATKTGENGPLPISHVPLVAGAAGGAALLLL-VFGVVGWVCHRRRQAKHSDTR 256
Qy 263 HPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPV 322

Db 190 GTNGKSSTTSPFVKDHSGSSTDG--SKAGHSSILGSEVALFAGIASGCIIFIVIIITLVV 247
 QY 248 AMCWRRRRRAKPSESRRHPGPGSFGRGGSGLGLGGGGMGPREAEPGELGIALRGGGAADPPF 307
 : ||| : :| | : | :|| :: || |
 Db 248 LLLKYRRRRHRKHSPQHTTTLSTLSTLATPKRSGNN----NGSEPSDIIPLR---TADSVF 300
 QY 308 CPHYEKVSGDYGHPVYIVQDGPPQSPNNIYY 338
 |||||: ||||
 Db 301 CPHYEKVSGDYGHPVYIVQEMPPQSPANIYY 331

RESULT 4

Q90Z33

ID Q90Z33 PRELIMINARY; PRT; 341 AA.
 AC Q90Z33;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Ephrin B1.
 GN EFNBL.
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21290827; PubMed=11397014;
 RA Chan J., Mably J.D., Serluca F.C., Chen J.N., Goldstein N.B.,
 RA Thomas M.C., Cleary J.A., Brennan C., Fishman M.C., Roberts T.M.;
 RT "Morphogenesis of prechordal plate and notochord requires intact
 RT eph/ephrin b signaling.";
 RL Dev. Biol. 234:470-482(2001).
 DR EMBL; AF375224; AAK64274.1; -.
 DR ZFIN; ZDB-GENE-010618-2; efnbl.
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR008972; Cupredoxin.
 DR InterPro; IPR001799; Ephrin.
 DR Pfam; PF00812; Ephrin; 1.
 DR PRINTS; PR01347; EPHRIN.
 DR ProDom; PD002533; Ephrin; 1.
 DR PROSITE; PS01299; EPHRIN; 1.
 SQ SEQUENCE 341 AA; 37849 MW; CB922F20E0D93E94 CRC64;

Query Match 24.8%; Score 607; DB 13; Length 341;
 Best Local Similarity 41.5%; Pred. NO. 3.5e-40;
 Matches 139; Conservative 49; Mismatches 109; Indels 38; Gaps 11;

Qy 24 LVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYL 83
 | : ||| | ||| | :| : | :||:|:|:|:|:| : | | |||||
 Db 23 LPAAKSLESVWNSQNPKFVSGKGLVIYPEIGDKLDIICPK---GDMGRP-YEFYKLYL 77
 Qy 84 VGGAQGRRC EAPPAPNLLLTCDRPDLDLRFITKFEYSPNLWGHEFRSHHDYIIATSDG 143
 | | | | :|:|:|:|:| :|:|:|:|:| | || : ||| :||:|
 Db 78 VKKEQAESCSTILDPNVLVTCNKPEKDIKFTIKFQEFSPNYMGLEFKRFTNYITSTNSG 137
 Qy 144 TREGLES LQGGVCLTRGMKVLLRVGQSPRG-----GAVPRKPVSEMPMERDRGAHSLEP 198

	: : : :	
Db	86 ETCHVTKSDMLLLNCDKPDQDVKFTEFKFQEFSPLNLWGLEFLRGKYHIISTSNSTFEGLD	145
Qy	150 SLQGGVCLTRGMKVLLRVGQSPRGGAV----PRKPVSEMPMERDRGAASLEPGKENLPG	205
	: : : : : : : :	
Db	146 NHHGGVCRSKSMKLVLVRVGQSPTDSFSAKNHPTRNPPKYPENKDQNTF-----SKENDVS	200
Qy	206 --DPTSNAISRGAEGPLPPPSMPAVALAGGLALLLVAGAGGAMCW-----RR	253
	: : :	
Db	201 QIDSMQNGESGGKSG-----ESVGSAGSDVALFAGV--ASGAVIFILIIIALVALLH	250
Qy	254 RRAKPSESRRHPGPSFGRGSLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEK	313
	: : : : : : : :	
Db	251 RRHQKHSACSGQLPLNLTLPKRSGSAGSSNNNGSEPDIIFPIRTSGSM---YCPHYEK	307
Qy	314 VSGDYGHVPVIYVDGPPQSPNIYY	338
	: :	
Db	308 VSGDYGHVPVIYVQEMPQNPNANIYY	332

RESULT 6

```

Q9W6H9
ID   Q9W6H9          PRELIMINARY;          PRT;    205 AA.
AC   Q9W6H9;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Ephrin-B2 (Fragment).
OS   Xenopus laevis (African clawed frog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC   Xenopodinae; Xenopus.
OX   NCBI_TaxID=8355;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97411149; PubMed=9259557;
RA   Smith A., Robinson V., Patel K., Wilkinson D.G.;
RT   "The EphA4 and EphB1 receptor tyrosine kinases and ephrin-B2 ligand
RT   regulate targeted migration of branchial neural crest cells.";
RL   Curr. Biol. 7:561-570(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=20099673;
RA   Helbling P.M., Saulnier D.M., Robinson V., Christiansen J.H.,
RA   Wilkinson D.G., Brandli A.W.;
RT   "Comparative analysis of embryonic gene expression defines potential
RT   interaction sites for Xenopus EphB4 receptors with ephrin-B ligands.";
RL   Dev. Dyn. 216:361-373(1999).
DR   EMBL; AF128844; AAD32610.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   InterPro; IPR008972; Cupredoxin.
DR   InterPro; IPR001799; Ephrin.
DR   Pfam; PF00812; Ephrin; 1.
DR   ProDom; PD002533; Ephrin; 1.
FT   NON_TER      1          1
SQ   SEQUENCE      205 AA;  22256 MW;  7DEDD34277260C87 CRC64;

```

Query Match 13.5%; Score 331; DB 13; Length 205;
 Best Local Similarity 36.4%; Pred. No. 1.7e-18;
 Matches 82; Conservative 35; Mismatches 72; Indels 36; Gaps 7;

```

QY      128 EFRSHHDYIIATSDGTREGLESIQGGVCLTRGMKVLLRVGQSP-----RGGAVPRKPVS 182
      ||:  |||||:|:|: ||::: :|||:|: ||:|:| || |  || : |:|
Db      1 EFQRDKDYIIISTSNGLSLEGVNQEGGVCVTAKMKILMKVGQDPNFHNHRGASSTRRPDH 60

QY      183 EMPM--ERDRGAAHSLEPGKENLPGDPTSNATSRGAEGPLPPSPMPAVAGAAGGLALLLL 240
      |   :   : |   |   : |   :|   :|   |   || | |   : :
Db      61 ESGTNGKSSTTSPHVNGPEGSSTEGKNAGHSSILGSEVAL-----FAGIASGSIIIFIV 113

QY      241 GVAGAGGAMCWRRRRRAKPSERHPGPGSFGRGGSLLGLG-----GGGGMGPREAEPGEL 293
      :   :   ||| :   :|   :|   |   |   |   :|| :
Db      114 IIITLVVLLKYYRRRHRKHSPQHT-----TSLSLSTLATPKRSGNNNG---SEPSDI 161

QY      294 GIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPSPQSPNIIY 338
      | ||   |: ||||| ||||| ||||| : |||| | |||
Db      162 IIPLR---TAEGVFCPHYEKVSGDYGHPVYIVQEMPPQSPANIIY 203
  
```

RESULT 7

Q9U3M2

```

ID  Q9U3M2          PRELIMINARY;      PRT;    237 AA.
AC  Q9U3M2;
DT  01-MAY-2000 (TrEMBLrel. 13, Created)
DT  01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT  01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE  C43F9.8 protein.
GN  C43F9.8.
OS  Caenorhabditis elegans.
OC  Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC  Rhabditidae; Peloderinae; Caenorhabditis.
OX  NCBI_TaxID=6239;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  Mortimore B.J.;
RL  Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
RN  [2]
RP  SEQUENCE FROM N.A.
RX  MEDLINE=99069613; PubMed=9851916;
RA  none;
RT  "Genome sequence of the nematode C.elegans: A platform for
RT  investigating biology.";
RL  Science 282:2012-2018(1998).
DR  EMBL; Z82262; CAB54195.1; -.
DR  PIR; T19914; T19914.
DR  WormPep; C43F9.8; CE23593.
DR  GO; GO:0016020; C:membrane; IEA.
DR  InterPro; IPR008972; Cupredoxin.
DR  InterPro; IPR001799; Ephrin.
DR  Pfam; PF00812; Ephrin; 1.
DR  PRINTS; PR01347; EPHRIN.
DR  ProDom; PD002533; Ephrin; 1.
SQ  SEQUENCE    237 AA;  26748 MW;  B9B2D9FCC71FE4FC CRC64;
  
```

Query Match 8.8%; Score 214.5; DB 5; Length 237;

Best Local Similarity 25.7%; Pred. No. 3.7e-09;
Matches 53; Conservative 41; Mismatches 83; Indels 29; Gaps 6;

```

QY      11 VRVGALLLLGVLGLVS-GLSLEPVYWNSANKRFQAEG-GYVLYPQIGDRLDLLCPRARPP 68
      ::  :|| :  :  : | | :|  |  :|:  |||: : ||::
Db      1 MQIATFILLSLFPFIGWARKIPDINWISSNPIFDVSNSTDHVISVHIGDRVSIRCPKSD 60

QY      69 GPHSSPNYEFYKLYLVGGAQGRRC EAPPAPNLLLTCDRPDLRLFTIKFQEYSPNLWGHE 128
      |  ||: :||:  :  |  |  | : ||  ::  | | : :|  | |
Db      61 G-----KYEYSYIYMVSDEEYDHCFL-SKPRLVGACDNQTINASINIVFRSFTPTPGGFE 114

QY      129 FRSHHDYIIA-----TSDGTREGLES LQGGVCLTRGMKVLLRVGQ 169
      |:  :|::|:  |||| ||::  : |:|  : ||:  |||
Db      115 FQPGKNYFLISKSEVDALIIYETANQIFPGTSDGTLEGIDRKKDGLCTAKQMKIKFEVGQ 174

QY      170 SPRGGAVPRKPVSEMPMERDRGAAHS 195
      ||  |:  :  ::|| | ||
Db      175 DRRGIENPK--FAARTLKKDRDAEHS 198

```

RESULT 8

Q9U474

```

ID   Q9U474          PRELIMINARY;          PRT;   279 AA.
AC   Q9U474;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   VAB-2 (Hypothetical protein Y37E11AR.6).
GN   VAB-2 OR Y37E11AR.6.
OS   Caenorhabditis elegans.
OC   Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC   Rhabditidae; Peloderinae; Caenorhabditis.
OX   NCBI_TaxID=6239;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=N2;
RX   MEDLINE=20084449; PubMed=10619431;
RA   Chin-Sang I.D., George S.E., Ding M., Moseley S.L., Lynch A.S.,
RA   Chisholm A.D.;
RT   "The ephrin VAB-2/EFN-1 functions in neuronal signaling to regulate
RT   epidermal morphogenesis in C. elegans.";
RL   Cell 99:781-790(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RX   MEDLINE=99069613; PubMed=9851916;
RA   None;
RT   "Genome sequence of the nematode C. elegans: a platform for
RT   investigating biology. The C. elegans Sequencing Consortium.";
RL   Science 282:2012-2018(1998).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Bristol N2;
RA   Miller N., Maggi L.;
RT   "The sequence of C. elegans cosmid Y37E11AR.";
RL   Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN   [4]

```


RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
 RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
 RA Patel S., Phouanenvong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.;
 RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF216287; AAF28394.1; -.
 DR EMBL; AE003843; AAF59335.2; -.
 DR EMBL; BT005199; AAO61756.1; -.
 DR FlyBase; FBgn0040324; Ephrin.
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR008972; Cupredoxin.

DR InterPro; IPR001799; Ephrin.
 DR Pfam; PF00812; Ephrin; 1.
 DR PRINTS; PR01347; EPHRIN.
 DR ProDom; PD002533; Ephrin; 1.
 SQ SEQUENCE 652 AA; 72302 MW; 5BA2F02F15964594 CRC64;

Query Match 7.8%; Score 192; DB 5; Length 652;
 Best Local Similarity 21.2%; Pred. No. 7.7e-07;
 Matches 103; Conservative 64; Mismatches 154; Indels 164; Gaps 22;

QY 33 VYWSANKRFQAEG-GYVLYPQIG-----DRLDLLCPRARPPGPHSSPNYEFYKLYLVG 85
 ::||::| | : : :: | | : : || | : | |
 Db 219 MHWNTSNSIFRIDNTDHIIDVKNKGNLAFEDQVHIICP-VYEPGTFENET-EKYIYNVS 276
 QY 86 GAQGRRCCEAPPA-PNLLLTCDRDLRLRFITKFEYSPNLWGHEFRSHHDYIIATSDGT 144
 : | | : : ||:| : ||| | : :| | || :||| | :|| :
 Db 277 KVEYETCRITNADPRVIAICDKPQKLMFFTITFRPFTPQPGGLEFLPGNDYYFISTS--S 334
 QY 145 REGLESQGGVCLTRGMKVLLRVGQSPRGGA VPRKPVSEMPMERDRGAAHSL-----EPG 199
 :: | || | | ||| : | : | : | | | : : :
 Db 335 KDDLYRRIGGRCSNMMKVVEFKVCCAPEDNN-KTTALSNSKSVTDTGGAINVNIANNDES 393
 QY 200 KENLPGDPTSNATSRGAEG-----PLPP-----P 223
 | | : : | : | | : | | | | | | | | | |
 Db 394 HVNSHGNIAIGTNIGINGGGQIIGGPQSAGIPINPLSGNNNINGIPTTINSNIDQFNRI 453
 QY 224 SMPAVAGAAGGLALLLLGVAGAGGAMCWRRRRAKPSERHPGPG-SFGRGGSGLGLGGGGG 282
 | : | | : | : | | : | | : | | | | | | | |
 Db 454 IQPNIIGNHVGTNAVGTGIVGGGGIIL-----TPGHAHGNINMLQPGRGGI 499
 QY 283 MGPRAEAPG----ELGIALRG-----GGAADPPFCPHYEKVSGDYGH 320
 | | | | : | : | | | | | | | | | | | |
 Db 500 NG---AYPGHHHIQTGIRINNVTQHNYPSHKGNANSNINGNDDH---HHYNK-----H 547
 QY 321 PVYIVQD-----GPPQSPNNIYYTSISVLEWPILHTIQLFFMRSKCSRVTTFLEFPVQV 373
 | : : : | | | | : | : | : | : | : | : | : | :
 Db 548 PNEVVKNEELTYNSGAATSDGNIFALWIWILS-----IFP--L 583
 QY 374 ITTSTCRMTSFSFTTLNPSMQACRAQMGEFRIRWCWFWDRLGTALFVLVLILLGLRLNM 433
 : : | : : : | | : | : | : | : | : | : | :
 Db 584 LSIQSCHLSSY-----WI-----SASFLVSTIALILGIHYL 613
 QY 434 HQTTL 438
 | |
 Db 614 IQITL 618

RESULT 10

Q98TZ1

ID Q98TZ1 PRELIMINARY; PRT; 202 AA.
 AC Q98TZ1;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Ephrin-A6 (Fragment).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Menzel P., Valencia F., Godement P., Dodelet V.C., Pasquale E.B.;
 RT "Ephrin-A6, a new ligand for EphA receptors in the developing visual
 RT system.";
 RL Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF317286; AAK00944.1; -.
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR008972; Cupredoxin.
 DR InterPro; IPR001799; Ephrin.
 DR Pfam; PF00812; Ephrin; 1.
 DR PRINTS; PR01347; EPHRIN.
 DR ProDom; PD002533; Ephrin; 1.
 DR PROSITE; PS01299; EPHRIN; 1.
 FT NON_TER 1 1
 SQ SEQUENCE 202 AA; 22624 MW; 91E2716FF91353F9 CRC64;

Query Match 7.3%; Score 178.5; DB 13; Length 202;
 Best Local Similarity 27.5%; Pred. No. 2.2e-06;
 Matches 56; Conservative 27; Mismatches 84; Indels 37; Gaps 7;

Qy 33 VYWNSANKRFQAEAGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRRC 92
 |||| :| || : | : | | ||: || | | : | :| |
 Db 25 VYWNGSNPRF-LQDDYSIQVSINDHLDIYCPHYSAPTPWA----ESFTLFMVDEEGYRGC 79
 Qy 93 EAPPAPNLLLTCDR---PDLDLRFITIKFQEYSPNLWGHEFRSHHDYIIAT-SDGTREGL 148
 | | :| : | :| | | :| | || | | : | :
 Db 80 SETPGAFKRWECKNPFAPFVPVRFSEKIQRFPTFSLGFEFRPGETYYYISVPTPGS---- 135
 Qy 149 ESLQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLPGDPT 208
 | || : | | | :| :| :| : | | |
 Db 136 ----AGRCLKLRSVCCR-----ASTPEPLTEVPNSQPRGR-----GGPE 171
 Qy 209 SNATSRGAEGPLPPPSMPAVAGAA 232
 :| | | :| | : |
 Db 172 GDAGSPRDAAPIPQRSRTLRVALA 195

RESULT 11

Q8N578

ID Q8N578 PRELIMINARY; PRT; 205 AA.
 AC Q8N578;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Ephrin-A1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Strausberg R.;

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 DR EMBL; AK009144; BAB26102.1; -.
 DR MGD; MGI:103236; Efnal.
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR008972; Cupredoxin.
 DR InterPro; IPR001799; Ephrin.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00812; Ephrin; 1.
 DR PRINTS; PR01347; EPHRIN.
 DR ProDom; PD002533; Ephrin; 1.
 DR PROSITE; PS01299; EPHRIN; 1.
 DR PROSITE; PS00678; WD_REPEATS_1; 1.
 SQ SEQUENCE 205 AA; 23772 MW; E37E55767459A4EC CRC64;

Query Match 6.8%; Score 167; DB 11; Length 205;
 Best Local Similarity 26.1%; Pred. No. 1.9e-05;
 Matches 43; Conservative 34; Mismatches 76; Indels 12; Gaps 4;

Qy 18 LLGVLGLVSGLSLEPVYWN SANKRFQ AEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYE 77
 |||: :: |::||:| ::| | ::|:| ||::|| : |
 Db 8 LLGLCCSLAAADRHIVFWNSSNPKFREE-DYTVHVQLNDYLDIICPHYEDDSV-ADAAME 65
 Qy 78 FYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDL---DLRFTIKFQEYSPNLWGHEFRSHHD 134
 | ||:| : |: : ||:| : ::||| ::| : | ||: |
 Db 66 RYTLYMVEHQEYVACQPQSKDQVRWNCNRPSAKHGPEKLSVKFQRFPTFILGKEFKEGHS 125
 Qy 135 YYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVPRK 179
 || |: :| || :| ::|:| ::|
 Db 126 YYYISKPIYHQE-----SQCLKLVTVNGKITHNPQAHVNPQE 163

RESULT 13

Q9CZS8

ID Q9CZS8 PRELIMINARY; PRT; 206 AA.
 AC Q9CZS8;
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE 10 days embryo cDNA, RIKEN full-length enriched library,
 DE clone:2610529M21, full insert sequence.
 GN EFNA4.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustinich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 DR EMBL; AK012195; BAB28092.1; -.
 DR MGD; MGI:106643; Efna4.
 DR GO; GO:0016020; C:membrane; IEA.
 DR InterPro; IPR008972; Cupredoxin.
 DR InterPro; IPR001799; Ephrin.
 DR Pfam; PF00812; Ephrin; 1.
 DR PRINTS; PR01347; EPHRIN.
 DR ProDom; PD002533; Ephrin; 1.
 DR PROSITE; PS01299; EPHRIN; 1.
 SQ SEQUENCE 206 AA; 22859 MW; 675E32971D1C6EBC CRC64;

Query Match 6.7%; Score 163.5; DB 11; Length 206;
 Best Local Similarity 28.1%; Pred. No. 3.6e-05;
 Matches 61; Conservative 17; Mismatches 80; Indels 59; Gaps 10;

QY 32 PVYWNSANKRFQAEAGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRR 91
 | : | | | : | | | | : | | | : | | | | : | | :
 Db 29 PIYWNSSNPRL-LRGDAVVELGFNDYLDIFCPHYESPGPPEGP--ETFALYIVDWSGYEA 85
 QY 92 CEAPPAPNL-LLTCDRPDL---DLRFITIKFQEYSPNLWGHEFRSHHDYIIATSDGTREG 147
 | | | : | | : | | | : | | | | | : | | :
 Db 86 CTAEGANSFQRWNC SMPFAPFSPVRFSEKIQRYPFPLGFEFLPGETYYYYISVPTPESPG 145
 QY 148 -LESLQGGVCLTRGMKVLLRVGQSPRGGA VPRKPVSEMPMERDRGA AH-SLEPGKENLPG 205
 | | | | : | | : | | : | | : | | :
 Db 146 RCLRLQVSVCC-----KESGSSHESAHP-----VG 170
 QY 206 DPTSNATS--RGAEGPLPPPSMPAVAGAAGGLALLLL 240
 | : | | | | | | | | | | | | | | | | | |
 Db 171 SPGESGTSGWRGGHAPSP-----LCLLLL 194

RESULT 14

Q9N178

ID Q9N178 PRELIMINARY; PRT; 675 AA.
 AC Q9N178;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Type X collagen.
 GN COL10A1.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21015405; PubMed=11130976;
 RA Nielsen V.H., Bendixen C., Arnbjerg J., Sorensen C.M., Jensen H.E.,
 RA Shukri N.M., Thomsen B.;
 RT "Abnormal growth plate function in pigs carrying a dominant mutation
 RT in type X collagen."
 RL Mamm. Genome 11:1087-1092(2000).
 DR EMBL; AF222861; AAF37271.1; -.
 DR InterPro; IPR001073; Clq.
 DR InterPro; IPR008161; Clg_helix.
 DR InterPro; IPR008160; Collagen.
 DR InterPro; IPR008983; TNF_like.
 DR Pfam; PF00386; Clq; 1.
 DR Pfam; PF01391; Collagen; 8.
 DR PRINTS; PR00007; COMPLEMNTC1Q.
 DR ProDom; PD000007; Clg_helix; 2.
 DR SMART; SM00110; ClQ; 1.
 DR PROSITE; PS01113; ClQ; 1.
 KW Collagen.
 SQ SEQUENCE 675 AA; 65447 MW; 26397B10310383F9 CRC64;

Query Match 6.3%; Score 155.5; DB 6; Length 675;
 Best Local Similarity 28.5%; Pred. No. 0.00064;
 Matches 103; Conservative 17; Mismatches 113; Indels 129; Gaps 25;

QY 1 MGPPHSGPGGVRVGALLLLGLVGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQI-GDR-L 58
 ||| |||
 Db 212 MGPP--GPPGV-----GKR--GENGFPGQPGIKGDRGF 240
 QY 59 DLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRR-CEAPPAPNLLLTCDRDLRLFTIKF 117
 | ||| | | || | || : | |
 Db 241 PGESGPAGPPGPQGP-----GEQGREGIGKPGAPG---AAGQPGL----- 278
 QY 118 QEYSPNLWGHEFRSHHDYIIATSDGT----REGLESLQGGVCLTRGMKVLLRVGQSPRG 173
 | || : | : || : | || | |
 Db 279 ----PGTKGHPGAPG-----MAGPPGAPGF GKPLGLKG----QRG-----PIG 315
 QY 174 GAVPRKPVSEMPMERDRG-AAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAA 232
 : | | : : : | | || | || : || | |
 Db 316 --LPGAPGA---KGEQGPAGHPGEPGLTGPPG-----SRGPQGPKGIPGNNGVPGPK 362
 QY 233 GGLALLLLGVAGAGGAMCWRRRR---AKPSESHPG-----PGSFGRGGSGLGLGGGGG 282

```

Db      363 GEIG--LAGPAGFPAGKGERGPSGLDGKPGYPGEPGLNGPKGNPGLPGPKGDPGIGGPPG 420
QY      283 M----GPRAE--PGELGIA-LRGG-----GAADPPFCPHYEKVSGDYGHVPYIVQDG 328
      :      || | : || | | ||      | || | :      || | : |
Db      421 LPGPVGPAGAKGVPGHNGEAGPRGAPGIPGTRGPIGPPGIPGFPGSKGDPGNP-----G 474
QY      329 PP 330
      ||
Db      475 PP 476

```

RESULT 15

O93431

```

ID      O93431      PRELIMINARY;      PRT;      229 AA.
AC      O93431;
DT      01-NOV-1998 (TrEMBLrel. 08, Created)
DT      01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Ephrin A-L1.
OS      Brachydanio rerio (Zebrafish) (Danio rerio).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC      Cyprinidae; Danio.
OX      NCBI_TaxID=7955;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Durbin L., Brennan C.H., Shiomi K., Cooke J.;
RT      "Eph signalling is required for segmentation and differentiation of
RT      the somites.";
RL      Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; AJ006838; CAA07264.1; -.
DR      GO; GO:0016020; C:membrane; IEA.
DR      InterPro; IPR008972; Cupredoxin.
DR      InterPro; IPR001799; Ephrin.
DR      InterPro; IPR003006; Ig_MHC.
DR      Pfam; PF00812; Ephrin; 1.
DR      PRINTS; PR01347; EPHRIN.
DR      ProDom; PD002533; Ephrin; 1.
DR      PROSITE; PS01299; EPHRIN; 1.
DR      PROSITE; PS00290; IG_MHC; 1.
SQ      SEQUENCE      229 AA;      26115 MW;      8684462F67AF6F5C CRC64;

```

```

Query Match      6.3%; Score 155; DB 13; Length 229;
Best Local Similarity 27.2%; Pred. No. 0.00019;
Matches 56; Conservative 23; Mismatches 93; Indels 34; Gaps 7;

```

```

QY      33 VYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRC 92
      |||| | | : | : :| | ||::||      | :|      | | ||:|      |
Db      25 VYWNSTNANFLWD-DYTVDVIRINDYLDIICPH-YAHGEIASQEAERYVLYMVELEDYENC 82
QY      93 EAPPAPNLLLTCDR---PDLDLRFTIKFQEYSPNLWGHEFRSHHDYIIATSDGTREGLE 149
      :      |      | | |      :| : ||| :| | |||      || | :      :
Db      83 KPHSFDQLRWECSRPFAPHAPEKFSEKFQRFPTFTLGKEFRQGESYYYIS-----K 133
QY      150 SL--QGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMPMERDRGAAHSLEPGKENLPGDP 207
      |      | ||      : | :      | |      :| | : :      : || :      || |

```

Db 134 PLHHHGQECLRLKVDVV-----GPHGSKNKKKMVEKVVEEIEGKMAAGGVHNPSNRLPADD 188
QY 208 TSNATSRGAEGPLPPPSMPAVAGAAG 233
| :| | : |
Db 189 -----PIAMIPVVQRSVG 201

Search completed: September 15, 2004, 12:39:12
Job time : 91.1384 secs

OM protein - protein search, using sw model

Run on: September 15, 2004, 12:22:15 ; Search time 17.7421 Seconds
(without alignments)
1335.348 Million cell updates/sec

Title: US-10-021-121-2
Perfect score: 2450
Sequence: 1 MGPPHSGPGGVRVGALLLLG.....TTLLRQRASVEAEAGQHGPL 455

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1841	75.1	340	1	EFB3_HUMAN	Q15768 homo sapien
2	1771	72.3	340	1	EFB3_MOUSE	O35393 mus musculu
3	628.5	25.7	336	1	EFB2_MOUSE	P52800 mus musculu
4	623	25.4	346	1	EFB1_HUMAN	P98172 homo sapien
5	620.5	25.3	333	1	EFB2_HUMAN	P52799 homo sapien
6	619	25.3	334	1	EFB1_CHICK	O73612 gallus gall
7	617.5	25.2	332	1	EFB2_BRARE	O73874 brachydanio
8	604.5	24.7	345	1	EFB1_MOUSE	P52795 mus musculu
9	599.5	24.5	345	1	EFB1_RAT	P52796 rattus norv
10	591	24.1	327	1	EFB1_XENLA	O13097 xenopus lae
11	185	7.6	195	1	EFA2_BRARE	P79727 brachydanio
12	179	7.3	238	1	EFA3_HUMAN	P52797 homo sapien
13	176	7.2	209	1	EFA2_MOUSE	P52801 mus musculu
14	175.5	7.2	213	1	EFA2_HUMAN	O43921 homo sapien
15	172	7.0	200	1	EFA2_CHICK	P52802 gallus gall
16	170.5	7.0	228	1	EFA5_CHICK	P52804 gallus gall
17	169.5	6.9	201	1	EFA4_HUMAN	P52798 homo sapien

18	169.5	6.9	228	1	EFA5_BRARE	P79728	brachydanio
19	167.5	6.8	216	1	EFA1_XENLA	P52794	xenopus lae
20	167.5	6.8	228	1	EFA5_HUMAN	P52803	homo sapien
21	167.5	6.8	228	1	EFA5_MOUSE	O08543	mus musculu
22	167.5	6.8	228	1	EFA5_RAT	P97605	rattus norv
23	166	6.8	205	1	EFA1_HUMAN	P20827	homo sapien
24	162.5	6.6	205	1	EFA1_RAT	P97553	rattus norv
25	161	6.6	205	1	EFA1_MOUSE	P52793	mus musculu
26	160.5	6.6	206	1	EFA4_MOUSE	O08542	mus musculu
27	159	6.5	680	1	CA1A_MOUSE	Q05306	mus musculu
28	154.5	6.3	1049	1	CA13_BOVIN	P04258	bos taurus
29	151.5	6.2	301	1	CC02_CAEEL	P17656	caenorhabdi
30	148.5	6.1	1670	1	CA34_HUMAN	Q01955	homo sapien
31	146.5	6.0	1774	1	CA1H_MOUSE	P39061	mus musculu
32	146	6.0	1027	1	CAFF_RIFPA	P30754	riftia pach
33	145	5.9	674	1	CA1A_BOVIN	P23206	bos taurus
34	145	5.9	1745	1	CA35_HUMAN	P25940	homo sapien
35	144.5	5.9	1516	1	CA1H_HUMAN	P39060	homo sapien
36	144	5.9	675	1	CA39_CHICK	P32017	gallus gall
37	144	5.9	921	1	CA19_HUMAN	P20849	homo sapien
38	143	5.8	674	1	CA1A_CHICK	P08125	gallus gall
39	142.5	5.8	635	1	CA28_HUMAN	P25067	homo sapien
40	142.5	5.8	1496	1	CA25_HUMAN	P05997	homo sapien
41	142	5.8	744	1	CA18_HUMAN	P27658	homo sapien
42	142	5.8	1029	1	CA26_MOUSE	Q02788	mus musculu
43	142	5.8	1763	1	CA24_ASCSU	P27393	ascaris suu
44	141.5	5.8	1466	1	CA13_HUMAN	P02461	homo sapien
45	141	5.8	744	1	CA18_RABIT	P14282	oryctolagus

ALIGNMENTS

RESULT 1

EFB3_HUMAN

ID EFB3_HUMAN STANDARD; PRT; 340 AA.
AC Q15768; O00680; Q8TBH7; Q92875;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ephrin-B3 precursor (EPH-related receptor tyrosine kinase ligand 8)
DE (LERK-8) (EPH-related receptor transmembrane ligand ELK-L3).
GN EFNB3 OR EPLG8 OR LERK8.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Cerretti D.P.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=97271551; PubMed=9126477;
RA Tang X.X., Pleasure D.E., Ikegaki N.;
RT "cdNA cloning, chromosomal localization, and expression pattern of

RT EPLG8, a new member of the EPLG gene family encoding ligands of EPH-
RT related protein-tyrosine kinase receptors.";
RL Genomics 41:17-24(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain cortex;
RX MEDLINE=96404527; PubMed=8808709;
RA Gale N.W., Flenniken A., Compton D.C., Jenkins N.A., Copeland N.G.,
RA Gilbert D.J., Davis S., Wilkinson D.G., Yancopoulos G.D.;
RT "Elk-L3, a novel transmembrane ligand for the Eph family of receptor
RT tyrosine kinases, expressed in embryonic floor plate, roof plate and
RT hindbrain segments.";
RL Oncogene 13:1343-1352(1996).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: May play a pivotal role in forebrain function. Binds to,
CC and induce the collapse of, commissural axons/growth cones in
CC vitro. May play a role in constraining the orientation of
CC longitudinally projecting axons (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Highly expressed in brain; expressed in
CC embryonic floor plate, roof plate and hindbrain segments.
CC -!- SIMILARITY: Belongs to the ephrin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U57001; AAB05170.1; -.
DR EMBL; U66406; AAC51203.1; -.
DR EMBL; U62775; AAC50707.1; -.

DR EMBL; BC022499; AAH22499.1; -.
 DR EMBL; BC042944; AAH42944.1; -.
 DR Genew; HGNC:3228; EFN3.
 DR MIM; 602297; -.
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0005005; F:transmembrane-ephrin receptor activity; TAS.
 DR GO; GO:0007267; P:cell-cell signaling; TAS.
 DR GO; GO:0007399; P:neurogenesis; TAS.
 DR InterPro; IPR008972; Cupredoxin.
 DR InterPro; IPR001799; Ephrin.
 DR Pfam; PF00812; Ephrin; 1.
 DR PRINTS; PR01347; EPHRIN.
 DR ProDom; PD002533; Ephrin; 1.
 DR PROSITE; PS01299; EPHRIN; 1.
 KW Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;
 KW Signal; Polymorphism.
 FT SIGNAL 1 27 POTENTIAL.
 FT CHAIN 28 340 EPHRIN-B3.
 FT DOMAIN 28 226 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 227 247 POTENTIAL.
 FT DOMAIN 248 340 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 338 340 PDZ RECOGNITION MOTIF (POTENTIAL).
 FT DISULFID 62 104 BY SIMILARITY.
 FT DISULFID 92 156 BY SIMILARITY.
 FT CARBOHYD 210 210 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARIANT 166 166 R -> Q.
 FT /FTId=VAR_002356.
 SQ SEQUENCE 340 AA; 35834 MW; EDFF2A23C2FDE79F CRC64;

Query Match 75.1%; Score 1841; DB 1; Length 340;
 Best Local Similarity 100.0%; Pred. No. 1e-113;
 Matches 338; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MGPPHSGPGGVRVGALLLLGLVGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL	60
Db	1	MGPPHSGPGGVRVGALLLLGLVGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL	60
Qy	61	LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRDLRFTIKFQEY	120
Db	61	LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRDLRFTIKFQEY	120
Qy	121	SPNLWGHEFRSHHDYIIATSDGTREGLESQGQVCLTRGMKVLLRVGQSPRGGA VPRKP	180
Db	121	SPNLWGHEFRSHHDYIIATSDGTREGLESQGQVCLTRGMKVLLRVGQSPRGGA VPRKP	180
Qy	181	VSEMPMERDRGAAHSLEPGKENLPGDPTS NATSRGAEGPLPPPSMPAVAGAAGGLALLLL	240
Db	181	VSEMPMERDRGAAHSLEPGKENLPGDPTS NATSRGAEGPLPPPSMPAVAGAAGGLALLLL	240
Qy	241	GVAGAGGAMCWRRRRAKPSERHPGPGSFGRGSLGLGGGGMGPREAEPGELGIALRGG	300
Db	241	GVAGAGGAMCWRRRRAKPSERHPGPGSFGRGSLGLGGGGMGPREAEPGELGIALRGG	300
Qy	301	GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY	338
Db	301	GAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIYY	338

RESULT 2

EFB3_MOUSE

ID EFB3_MOUSE STANDARD; PRT; 340 AA.
AC O35393;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ephrin-B3 precursor.
GN EFNB3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98143367; PubMed=9484836;
RA Bergemann A.D., Zhang L., Chiang M.-K., Brambilla R., Klein R.,
RA Flanagan J.G.;
RT "Ephrin-B3, a ligand for the receptor EphB3, expressed at the midline
RT of the developing neural tube.";
RL Oncogene 16:471-480(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [3]
RP FUNCTION.
RX MEDLINE=20171264; PubMed=10704386;
RA Imondi R., Wideman C., Kaprielian Z.;
RT "Complementary expression of transmembrane ephrins and their receptors
RT in the mouse spinal cord: a possible role in constraining the
RT orientation of longitudinally projecting axons.";
RL Development 127:1397-1410(2000).
CC -!- FUNCTION: May play a pivotal role in forebrain function. Binds to,
CC and induce the collapse of, commissural axons/growth cones in


```

CC      vitro. May play a role in constraining the orientation of
CC      longitudinally projecting axons.
CC      -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC      -!- TISSUE SPECIFICITY: Expressed on lateral floor plate cells,
CC      specifically on commissural axon segments that have passed through
CC      the floor plate. Expressed in cells of the retinal ganglion cell
CC      layer during retinal axon guidance to the optic disk.
CC      -!- DEVELOPMENTAL STAGE: Expressed in the floor plate throughout the
CC      period of commissural axon pathfinding.
CC      -!- SIMILARITY: Belongs to the ephrin family.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF025288; AAC53537.1; -.
DR      EMBL; BC052001; AAH52001.1; -.
DR      EMBL; BC058617; AAH58617.1; -.
DR      MGD; MGI:109196; Efnb3.
DR      GO; GO:0007628; P:adult walking behavior; IMP.
DR      GO; GO:0007411; P:axon guidance; IMP.
DR      InterPro; IPR008972; Cupredoxin.
DR      InterPro; IPR001799; Ephrin.
DR      Pfam; PF00812; Ephrin; 1.
DR      PRINTS; PR01347; EPHRIN.
DR      ProDom; PD002533; Ephrin; 1.
DR      PROSITE; PS01299; EPHRIN; 1.
KW      Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;
KW      Signal.
FT      SIGNAL          1      27      POTENTIAL.
FT      CHAIN           28     340     EPHRIN-B3.
FT      DOMAIN          28     227     EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM        228    248     POTENTIAL.
FT      DOMAIN          249    340     CYTOPLASMIC (POTENTIAL).
FT      DOMAIN          338    340     PDZ RECOGNITION MOTIF (POTENTIAL).
FT      DISULFID         62    104     BY SIMILARITY.
FT      DISULFID         92    156     BY SIMILARITY.
FT      CARBOHYD        210    210     N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ      SEQUENCE      340 AA;  35884 MW;  52F3D58FD209A6B8 CRC64;

Query Match          72.3%; Score 1771; DB 1; Length 340;
Best Local Similarity 95.6%; Pred. No. 3.9e-109;
Matches 323; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

Qy      1 MGPPHSGPGGVVRGALLLLGLVGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60
      || || |||||:||||||| |||||
Db      1 MGAPHFGPGGVQVGALLLLGFAGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDL 60

Qy      61 LCPRARPPGPHSSPNYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120
      |||||:||||||| |||||
Db      61 LCPRARPPGPHSSPSYEFYKLYLVEGAQGRRCCEAPPAPNLLLTCDRPDLDLRFTIKFQEY 120

Qy      121 SPNLWGHEFRSHHDYIIATSDGTREGLESLQGGVCLTRGMKVLLRVGQSPRGGA VPRKP 180

```


RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP FUNCTION.
 RX MEDLINE=20171264; PubMed=10704386;
 RA Imondi R., Wideman C., Kaprielian Z.;
 RT "Complementary expression of transmembrane ephrins and their receptors
 RT in the mouse spinal cord: a possible role in constraining the
 RT orientation of longitudinally projecting axons.";
 RL Development 127:1397-1410(2000).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (1.92 ANGSTROMS) OF 30-170.
 RX MEDLINE=21563306; PubMed=11703926;
 RA Toth J., Cutforth T., Gelinas A.D., Bethoney K.A., Bard J.,
 RA Harrison C.J.;
 RT "Crystal structure of an ephrin ectodomain.";
 RL Dev. Cell 1:83-92(2001).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 31-168 IN COMPLEX WITH
 RP EPHB2.
 RX MEDLINE=21638766; PubMed=11780069;
 RA Himanen J.-P., Rajashankar K.R., Lackmann M., Cowan C.A.,
 RA Henkemeyer M., Nikolov D.B.;
 RT "Crystal structure of an Eph receptor-ephrin complex.";
 RL Nature 414:933-938(2001).
 CC -!- FUNCTION: Binds to the receptor tyrosine kinases EPHB2 and EPHB4.
 CC May play a role in constraining the orientation of longitudinally
 CC projecting axons.
 CC -!- SUBUNIT: Binds to the receptor tyrosine kinase EPHB4.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed on lateral floor plate cells,
 CC specifically on commissural axon segments that have passed through
 CC the floor plate. Expressed in cells of the retinal ganglion cell
 CC layer during retinal axon guidance to the optic disk.
 CC -!- DEVELOPMENTAL STAGE: Expressed in the floor plate throughout the

CC period of commissural axon pathfinding.
 CC -!- PTM: Inducible phosphorylation of tyrosine residues in the
 CC cytoplasmic domain (By similarity).
 CC -!- SIMILARITY: Belongs to the ephrin family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U16819; AAA99708.1; -.
 DR EMBL; L38847; AAC42052.1; -.
 DR EMBL; U30244; AAA82934.1; -.
 DR EMBL; BC057009; AAH57009.1; -.
 DR PIR; I49766; I49766.
 DR PDB; 1IKO; 15-MAY-02.
 DR PDB; 1KGY; 28-MAY-02.
 DR MGD; MGI:105097; Efnb2.
 DR InterPro; IPR008972; Cupredoxin.
 DR InterPro; IPR001799; Ephrin.
 DR Pfam; PF00812; Ephrin; 1.
 DR PRINTS; PR01347; EPHRIN.
 DR ProDom; PD002533; Ephrin; 1.
 DR PROSITE; PS01299; EPHRIN; 1.
 KW Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;
 KW Signal; Phosphorylation; 3D-structure.
 FT SIGNAL 1 28 POTENTIAL.
 FT CHAIN 29 336 EPHRIN-B2.
 FT DOMAIN 29 232 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 233 253 POTENTIAL.
 FT DOMAIN 254 336 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 334 336 PDZ RECOGNITION MOTIF (POTENTIAL).
 FT DISULFID 65 104
 FT DISULFID 92 156
 FT CARBOHYD 39 39 N-LINKED (GLCNAC. . .).
 FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 3 4 MISSING (IN REF. 3).
 FT CONFLICT 177 177 A -> T (IN REF. 1).
 SQ SEQUENCE 336 AA; 37202 MW; D08894996E399554 CRC64;

Query Match 25.7%; Score 628.5; DB 1; Length 336;
 Best Local Similarity 41.8%; Pred. No. 2.3e-34;
 Matches 137; Conservative 49; Mismatches 129; Indels 13; Gaps 5;

Qy 14 GALLLLGVLGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
 | |::| : : |||:||||:| :| | |||||:|::|: :
 Db 17 GLLMVLCRTAISRSIVLEPIYWSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 73
 Qy 74 PNYEFYKLYLVGGAQGRRCAPPAPNLLLTCDRDLRLFTIKFQEYSPNLWGHEFRSHH 133
 ||::|:|:| | || || | || |::|:|||||:||||| ||: :
 Db 74 GQYEYYKVYMVVDKQADRCTIKKENTPLNLCARPDQDVKFTIKFQEFSPNLWGLEFQKNK 133
 Qy 134 DYYIIATSDGTREGLESQGVCVLTGRMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
 ||||:|::|: ||::: |||| || ||:|:|||| | | | :|

Db 134 DYYIISTSNGLSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSARNHGPTRRPELEAGTN 193

QY 191 GAAHSLEPGKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
| : : | : | | : : : | : | | : : : :

Db 194 GRSSTTSPFVKPNPGSSTDGNSAGHSNNLLGSEVALFAGIASGCIIFIVIIITLVVLLL 253

QY 251 WRRRRRAKPSESRHPGPGSFRGGSLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
| | | : : | : | : | | : | | | | | | |

Db 254 KYRRRHRKHSPQHTTTLSLSTLATPKRGGNN----NGSEPSDVIIPLR---TADSVFCPH 306

QY 311 YEKVSGDYGHPVYIVQDGPQSPNNIYY 338
| | | | | | | | | | | : | | | | | | |

Db 307 YEKVSGDYGHPVYIVQEMPQSPANNIYY 334

RESULT 4

EFB1_HUMAN

ID EFB1_HUMAN STANDARD; PRT; 346 AA.

AC P98172;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Ephrin-B1 precursor (EPH-related receptor tyrosine kinase ligand 2)

DE (LERK-2) (ELK ligand) (ELK-L).

GN EFNBI OR EPLG2 OR LERK2 OR EFL-3.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Placenta;

RX MEDLINE=94349923; PubMed=8070404;

RA Beckmann M.P., Cerretti D.P., Baum P., Vanden Bos T., James L.,

RA Farrah T., Kozlosky C., Hollingsworth T., Shilling H., Maraskovsky E.,

RA Fletcher F.A., Lhotak V., Pawson T., Lyman S.D.;

RT "Molecular characterization of a family of ligands for eph-related

RT tyrosine kinase receptors.";

RL EMBO J. 13:3757-3762(1994).

RN [2]

RP SEQUENCE FROM N.A.

RA Davis S., Gale N.W., Aldrich T.H., Maisonpierre P.C., Lhotak V.,

RA Pawson T., Goldfarb M., Yancopoulos G.D.;

RL Submitted (NOV-1994) to the EMBL/GenBank/DDBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RA Fletcher F.A., Huebner K., Shaffer L.G., Monaco A., Mueller U.,

RA Kozlosky C., Druck T., Simoneaux D.K., Fairweather N., Chelly J.,

RA Cerretti D.P., Belmont J.W., Beckmann M.P., Lyman S.D.;

RL Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RA Howden P.;

RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

RN [5]

RP SEQUENCE FROM N.A.

RC TISSUE=Eye, and Skin;

RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Binds to the receptor tyrosine kinases EPHB1 and EPHA1.
 CC Binds to, and induce the collapse of, commissural axons/growth
 CC cones in vitro. May play a role in constraining the orientation of
 CC longitudinally projecting axons (By similarity).
 CC -!- SUBUNIT: Binds GRIP1 and GRIP2.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Heart, placenta, lung, liver, skeletal muscle,
 CC kidney, pancreas.
 CC -!- INDUCTION: By TNF-alpha.
 CC -!- PTM: Inducible phosphorylation of tyrosine residues in the
 CC cytoplasmic domain (By similarity).
 CC -!- SIMILARITY: Belongs to the ephrin family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U09304; AAA53093.1; -.
 DR EMBL; L37361; AAA52369.1; -.
 DR EMBL; U09303; AAB41127.1; -.
 DR EMBL; AL136032; -; NOT_ANNOTATED_CDS.
 DR EMBL; BC016649; AAH16649.1; -.
 DR EMBL; BC052979; AAH52979.1; -.
 DR PIR; S46993; S46993.
 DR Genew; HGNC:3226; EFNBL1.
 DR MIM; 300035; -.
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0005625; C:soluble fraction; TAS.
 DR GO; GO:0005108; F:transmembrane ephrin; TAS.
 DR GO; GO:0007155; P:cell adhesion; TAS.
 DR GO; GO:0007267; P:cell-cell signaling; TAS.
 DR InterPro; IPR008972; Cupredoxin.

DR InterPro; IPR001799; Ephrin.
 DR Pfam; PF00812; Ephrin; 1.
 DR PRINTS; PR01347; EPHRIN.
 DR ProDom; PD002533; Ephrin; 1.
 DR PROSITE; PS01299; EPHRIN; 1.
 KW Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;
 KW Signal; Phosphorylation.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 346 EPHRIN-B1.
 FT DOMAIN 25 237 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 238 258 POTENTIAL.
 FT DOMAIN 259 346 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 344 346 PDZ RECOGNITION MOTIF (POTENTIAL).
 FT DISULFID 64 101 BY SIMILARITY.
 FT DISULFID 89 153 BY SIMILARITY.
 FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 346 AA; 38006 MW; 473DD2F1A5BF89DE CRC64;

Query Match 25.4%; Score 623; DB 1; Length 346;
 Best Local Similarity 39.2%; Pred. No. 5.4e-34;
 Matches 143; Conservative 48; Mismatches 116; Indels 58; Gaps 9;

Qy 8 PGGVRVGALLLLGVLGLVSGL-----SLEPVYWNSANKRFQAEGGYVLYPQIGDRDL 61
 || :| |: |: : | :||| |:| |:| :| :| |:|:| |:|:|
 Db 4 PGQRWL GKVLVAMVWALCRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDII 63
 Qy 62 CPRARPPGPHSSPNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRPDLRLFTIKFQEYS 121
 |||| | :|:|:| | | :|:|:|:|:| :|:|:|:|:|
 Db 64 CPRAEAGRP-----YEYKLYLVRPEQAAACSTVLDPNVLVTCNRPEQEIRFTIKFQEFS 118
 Qy 122 PNLWGHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVPRKPV 181
 || | |:| |:|:| :|:|:| |:|:| :|:| | | |:|:|:| | :
 Db 119 PNYMGLEFKKHHDYIITSTSNGLSLEGLNREGGVCRTRTMKIIMKVGQDPNAVTPQLTT 178
 Qy 182 SEMP MERDRGAHSLE-PGKENLPGDPTS NATSRGAEGPLPPPSMPAVAGAAGGLA---- 236
 | | | : : || | | : | | | |:|:| :
 Db 179 SRPSKEADNTVKMATQAPGSRGSLGSDGKHETVNQEEKSGP-----GASGGSSGDPD 231
 Qy 237 -----LLLLGVAGAGGA-----MCWRRRRRAKPSES RHPGPGSFGRGGS LGL 277
 : | || | :|:| | :| | :| |
 Db 232 GFFNSKVALFAAVGAGCVIFLLIIIFLTVLL LKLRKRHRKHTQQ-----RAAALSL 282
 Qy 278 ----GGGGMGPREAEPGELGIALRGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSP 333
 || | || :|:| | : :|:|:|:|:|:|:|:|:|:|:|:|:|
 Db 283 STLASPKGSGTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSP 339
 Qy 334 PNIIY 338
 ||||
 Db 340 ANIIY 344

RESULT 5

EFB2_HUMAN

ID EFB2_HUMAN STANDARD; PRT; 333 AA.
 AC P52799;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Ephrin-B2 precursor (EPH-related receptor tyrosine kinase ligand 5)
 DE (LERK-5) (HTK ligand) (HTK-L).
 GN EFNB2 OR EPLG5 OR LERK5 OR HTKL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=96145238; PubMed=8559144;
 RA Cerretti D.P., Vanden Bos T., Nelson N., Kozlosky C.J., Reddy P.,
 RA Maraskovsky E., Park L.S., Lyman S.D., Copeland N.G., Gilbert D.J.,
 RA Jenkins N.A., Fletcher R.A.;
 RT "Isolation of LERK-5: a ligand of the eph-related receptor tyrosine
 RT kinases.";
 RL Mol. Immunol. 32:1197-1205(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=95199254; PubMed=7534404;
 RA Bennett B.D., Zeigler F.C., Gu Q., Fendly B., Goddard A.D.,
 RA Gillett N., Matthews W.;
 RT "Molecular cloning of a ligand for the EPH-related receptor protein-
 RT tyrosine kinase Htk.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:1866-1870(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98192220; PubMed=9533549;
 RA Vogt T., Stolz W., Welsh J., Jung B., Kerbel R.S., Kobayashi H.,
 RA Landthaler M., McClelland M.;
 RT "Overexpression of Lerk-5/Eplg5 messenger RNA: a novel marker for
 RT increased tumorigenicity and metastatic potential in human malignant
 RT melanomas.";
 RL Clin. Cancer Res. 4:791-797(1998).
 CC -!- FUNCTION: Binds to the receptor tyrosine kinases EPHB4 and EPHA3.
 CC May play a role in constraining the orientation of longitudinally
 CC projecting axons (By similarity).
 CC -!- SUBUNIT: Binds to the receptor tyrosine kinases EPHB4 and EPHA3.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Lung and kidney.
 CC -!- PTM: Inducible phosphorylation of tyrosine residues in the
 CC cytoplasmic domain (By similarity).
 CC -!- SIMILARITY: Belongs to the ephrin family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U16797; AAA99707.1; -.
 DR EMBL; L38734; AAC41752.1; -.
 DR EMBL; U81262; AAD03786.1; -.

DR PIR; I84743; I84743.
 DR Genew; HGNC:3227; EFNB2.
 DR MIM; 600527; -.
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.
 DR GO; GO:0005106; F:ephrin; TAS.
 DR GO; GO:0005108; F:transmembrane ephrin; TAS.
 DR GO; GO:0007267; P:cell-cell signaling; TAS.
 DR GO; GO:0007397; P:histogenesis and organogenesis; TAS.
 DR InterPro; IPR008972; Cupredoxin.
 DR InterPro; IPR001799; Ephrin.
 DR Pfam; PF00812; Ephrin; 1.
 DR PRINTS; PR01347; EPHRIN.
 DR ProDom; PD002533; Ephrin; 1.
 DR PROSITE; PS01299; EPHRIN; 1.
 KW Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;
 KW Signal; Phosphorylation.
 FT SIGNAL 1 27 POTENTIAL.
 FT CHAIN 28 333 EPHRIN-B2.
 FT DOMAIN 28 229 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 230 250 POTENTIAL.
 FT DOMAIN 251 333 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 331 333 PDZ RECOGNITION MOTIF (POTENTIAL).
 FT DISULFID 62 101 BY SIMILARITY.
 FT DISULFID 89 153 BY SIMILARITY.
 FT CARBOHYD 36 36 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 333 AA; 36923 MW; 6D9932A632626AEA CRC64;

Query Match 25.3%; Score 620.5; DB 1; Length 333;
 Best Local Similarity 40.5%; Pred. No. 7.6e-34;
 Matches 133; Conservative 52; Mismatches 130; Indels 13; Gaps 5;

Qy 14 GALLLLGLVGLVSGLSLEPVYWN SANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
 | |::| : : ||:||||:| :| | |||||::|::|: :
 Db 14 GVLMLCRTAISKSIVLEPIYWNSSNSKFLPGQGLVLYPQIGDKLDIICPKV---DSKTV 70
 Qy 74 PNYEFYKLYLVGGAQGRRC EAPPAPNLLLLTCDRPDLDLRFITKFQEYSPNLWGHEFRSHH 133
 ||:|::|:| | || || | :|| |::| |||||:| ||||| ||: :
 Db 71 GQYEYYKVYMVDDKDQADRCTIKKENTPLLNCAPDQDIKFTIKFQEFSPNLWGLEFQKNK 130
 Qy 134 DYYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQ--SPRGGAVPRKPVSEMPMER-DR 190
 ||||:|::|:| ||:: :||| || ||:|::||| | | : | :|
 Db 131 DYYIISTSNGLSLEGLDNQEGGVCQTRAMKILMKVGQDASSAGSTRNKDPTRRPELEAGTN 190
 Qy 191 GAAHSLEPGKENLPGDPTS NATSRGAEGPLPPPSMPAVAGAAGGLALLLLGVAGAGGAMC 250
 | : : | : || | : : : : : || | | : : : :
 Db 191 GRSSTTSPFVKPNPGSSTDGNSAGHSGNNILGSEVALFAGIASGCIIFIVIIITLVVLLL 250
 Qy 251 WRRRRRAKPSES RHPGPGSFGRGGS LGLGGGGMGPREAEPGELGIALRGGGAADPPFCPH 310
 ||| : :| | : | : || :||:| || || |||
 Db 251 KYRRRHRKHSPQHTTTLSTLATPKRSGNN---NGSEPSDIIIPLR---TADSVFCPH 303
 Qy 311 YEKVSGDYGHPVYIVQDGPPQSPPNIYY 338
 ||||| |||||: ||||| ||||
 Db 304 YEKVSGDYGHPVYIVQEMPPQSPANIYY 331

RESULT 6

EFB1_CHICK

ID EFB1_CHICK STANDARD; PRT; 334 AA.
 AC 073612;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Ephrin-B1 precursor (CEK5 ligand) (CEL5-L).
 GN EFNBL.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97223524; PubMed=9070326;
 RA Holash J.A., Soans C., Chong L.D., Shao H., Dixit V.M.,
 RA Pasquale E.B.;
 RT "Reciprocal expression of the Eph receptor Cek5 and its ligand(s) in
 RT the early retina.";
 RL Dev. Biol. 182:256-269(1997).
 CC -!- SUBUNIT: Binds to the receptor tyrosine kinase EPHB2.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- PTM: Inducible phosphorylation of tyrosine residues in the
 CC cytoplasmic domain (By similarity).
 CC -!- SIMILARITY: Belongs to the ephrin family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U72394; AAC07986.1; -.
 DR InterPro; IPR008972; Cupredoxin.
 DR InterPro; IPR001799; Ephrin.
 DR Pfam; PF00812; Ephrin; 1.
 DR PRINTS; PR01347; EPHRIN.
 DR ProDom; PD002533; Ephrin; 1.
 DR PROSITE; PS01299; EPHRIN; 1.
 KW Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;
 KW Signal; Phosphorylation.
 FT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 334 EPHRIN-B1.
 FT DOMAIN 26 231 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 232 252 POTENTIAL.
 FT DOMAIN 253 334 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 332 334 PDZ RECOGNITION MOTIF (POTENTIAL).
 FT DISULFID 60 97 BY SIMILARITY.
 FT DISULFID 85 149 BY SIMILARITY.
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 334 AA; 36858 MW; 48AF556E9ED56CD5 CRC64;

Query Match

25.3%; Score 619; DB 1; Length 334;

Best Local Similarity 39.3%; Pred. No. 9.5e-34;
Matches 144; Conservative 50; Mismatches 100; Indels 72; Gaps 13;

```

Qy      8 PGGVR--VGALLLLGLVGLVSGLSLEPVYWNSANKRFQAEGGYVLYPQIGDRDLDCPRA 65
      | | | :| || | | | |||| |:: | :| : | |::|||:|::|:|:|
Db      4 PRGGRWLLGVLLALCRLAAPLAKSLEPVSWNSAGNPKFMSGKGLVIYPEIGDKLDIICPKA 63

Qy     66 RPPGPHSSPNYEFYKLYLVGGAQGRRCAPPAPNLLLTCDRDLRFTIKFQEYSPNLW 125
      | | | |::||| | | | |::|||:|:|:|:|:|:|:|:|:|:|:|:|
Db     64 EPSKP-----YDYKLYLVKKDQADACSTVMDPNVLVTCNRPEQEIRFTIKFQEFSPNYM 118

Qy    126 GHEFRSHHDYIIATSDGTREGLESIQGGVCLTRGMKVLLRVGQSPRGAVPRKPVSEMP 185
      | ||: ||:| :||:| :||:| :||| || ||:::| | | :| : : |
Db    119 GLEFKRQDYFITSTSNGLDGLNREGGVCQTRSMKIVMKVGQDP-NAVIPEQLTTSRP 177

Qy    186 MER-----DRGAAHSL----EPGKENLPGDPTSNA--TSRGAEGPLPPPSMPAVAGA 231
      : : | : ||| || | | :| | | | |
Db    178 SKEADNTVKIVTQSPRHKVPTVEEPGK---PGSVNQNGQETQGPSDGFL--SSKVAVFAA 232

Qy    232 AGG-----LALLLLGVAGAGGAMCWRRRRAKPSESRL-----PGPGSFGRG 272
      | | | |::: | | | |:: | | | |
Db    233 IGAGCVIFILIIIFLVLLIKI-----RKRHRKHTQQRAAALSSTLASPKCSGNA 283

Qy    273 GSLGLGGGGMGPREAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQS 332
      || | |:: | | | : |||||:| | | |
Db    284 GS-----EPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQS 326

Qy    333 PPNIYY 338
      | |||
Db    327 PANIYY 332

```

RESULT 7

EFB2_BRARE

```

ID   EFB2_BRARE          STANDARD;          PRT;   332 AA.
AC   073874;
DT   15-JUL-1999 (Rel. 38, Created)
DT   15-JUL-1999 (Rel. 38, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Ephrin-B2 precursor (Ephrin B2a).
GN   EFNB2 OR EFNB2A.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=98438455; PubMed=9765210;
RA   Durbin L., Brennan C., Shiomi K., Cooke J., Barrios A.,
RA   Shanmugalingam S., Guthrie B., Lindberg R., Holder N.;
RT   "Eph signaling is required for segmentation and differentiation of
RT   the somites.";
RL   Genes Dev. 12:3096-3109(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21290827; PubMed=11397014;

```

RA Chan J., Mably J.D., Serluca F.C., Chen J.N., Goldstein N.B.,
 RA Thomas M.C., Cleary J.A., Brennan C., Fishman M.C., Roberts T.M.;
 RT "Morphogenesis of prechordal plate and notochord requires intact
 RT eph/ephrin b signaling.";
 RL Dev. Biol. 234:470-482(2001).
 CC -!- SUBUNIT: Binds to the receptor tyrosine kinase EPHB4.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- PTM: Inducible phosphorylation of tyrosine residues in the
 CC cytoplasmic domain (By similarity).
 CC -!- SIMILARITY: Belongs to the ephrin family.

CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----

DR EMBL; AJ004863; CAA06168.1; -.
 DR EMBL; AF375225; AAK64275.1; -.
 DR ZFIN; ZDB-GENE-990415-67; efnb2a.
 DR InterPro; IPR008972; Cupredoxin.
 DR InterPro; IPR001799; Ephrin.
 DR Pfam; PF00812; Ephrin; 1.
 DR PRINTS; PR01347; EPHRIN.
 DR ProDom; PD002533; Ephrin; 1.
 DR PROSITE; PS01299; EPHRIN; 1.
 KW Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;
 KW Signal; Phosphorylation.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 332 EPHRIN-B2.
 FT DOMAIN 25 225 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 226 246 POTENTIAL.
 FT DOMAIN 247 332 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 330 332 PDZ RECOGNITION MOTIF (POTENTIAL).
 FT DISULFID 59 98 BY SIMILARITY.
 FT DISULFID 86 150 BY SIMILARITY.
 FT CARBOHYD 20 20 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 33 33 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 136 136 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 211 211 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 332 AA; 36724 MW; 189ED82372C71C8B CRC64;

Query Match 25.2%; Score 617.5; DB 1; Length 332;
 Best Local Similarity 41.8%; Fred. No. 1.2e-33;
 Matches 143; Conservative 54; Mismatches 106; Indels 39; Gaps 12;

Qy 14 GALLLLGVLGLVSGLSLEPVYWSANKRFQAEGGYVLYPQIGDRLDLLCPRARPPGPHSS 73
 | |:: : | | : :||: | : | | | | | : : : | |
 Db 11 GVLVIACKVNLSRALILDSIYWNTTNTKFPVPGQGLVLYPQIGDKMDIVCPVE---GGSM 67
 Qy 74 PNYEFYKLYLVGGAQGRRCEAPPAPNLLLTCDRDLRLFTIKFQEYSPNLWGHEFRSHH 133
 | : | | | : | : | : | | : | | : : | | | : | | | | |
 Db 68 EGVEYYKLYMVPLEQLKSCQVTKADTPLLNCVKPDQDVKFTLKFQEFSPNLWGLEFFRGK 127
 Qy 134 DYYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGAVPRK-PVSEMPMERDRGA 192

```

      |||||:||||| |||:: |||| | : ||::|||:| | : | | | | |
Db      128 DYYIIISTSNGTMEGLDNQEGGVCKTKSMKIIMKVGQNPSDPISPKDYPTSYPPKHPDLGG 187
Qy      193 AHS-----LEP-----GKENLPGDPTSNATSRGAEGPLPPPSMPAVAGAAGGLALLLLGV 242
      | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      188 KDSKSNEVLKPDASPHGEDK--GDGNKSSSVIGSEVAL----FACIASASVIVIIIIIML 241
Qy      243 AGAGGAMCWRRRRRAKPSESRHPGPGSFG-----RGGSLGLGGGGMGPREAEPGELGIA 296
      : : ||| | | : | | | | | | | | | | | | | | | |
Db      242 VFL--LLKYRRRHRKHS-PQHATTLSLSTLATPKRGGS----GGNNNG---SEPSDIIIP 291
Qy      297 LRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPQPSPNIYY 338
      || || ||||| ||||| ||||| ||||| ||||| |||||
Db      292 LR---TADSVFCPHYEKVSGDYGHPVYIVQEMPQPSPANIYY 330

```

RESULT 8

EFB1_MOUSE

```

ID      EFB1_MOUSE          STANDARD;          PRT;    345 AA.
AC      P52795;
DT      01-OCT-1996 (Rel. 34, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DT      15-MAR-2004 (Rel. 43, Last annotation update)
DE      Ephrin-B1 precursor (EPH-related receptor tyrosine kinase ligand 2)
DE      (LERK-2) (ELK ligand) (ELK-L) (STRA1 protein) (CEK5 receptor ligand)
DE      (CEK5-L).
GN      EFN1 OR EPLG2 OR LERK2 OR STRA1 OR EPL2.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=129/Sv;
RX      MEDLINE=95203867; PubMed=7896266;
RA      Fletcher F.A., Renshaw B., Hollingsworth T., Baum P., Lyman S.D.,
RA      Jenkins N.A., Gilbert D.J., Copeland N.G., Davison B.L.;
RT      "Genomic organization and chromosomal localization of mouse Eplg2, a
RT      gene encoding a binding protein for the receptor tyrosine kinase
RT      elk.";
RL      Genomics 24:127-132(1994).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=95377533; PubMed=7649373;
RA      Bouillet P., Oulad-Abdelghani M., Vicaire S., Garnier J.M.,
RA      Schuhbaur B., Dolle P., Chambon P.;
RT      "Efficient cloning of cDNAs of retinoic acid-responsive genes in P19
RT      embryonal carcinoma cells and characterization of a novel mouse gene,
RT      Stra1 (mouse LERK-2/Eplg2).";
RL      Dev. Biol. 170:420-433(1995).
RN      [3]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Brain;
RX      MEDLINE=95014510; PubMed=7929389;
RA      Shao H., Lou L., Pandey A., Pasquale E.B., Dixit V.M.;
RT      "cDNA cloning and characterization of a ligand for the Cek5 receptor
RT      protein-tyrosine kinase.";

```

RL J. Biol. Chem. 269:26606-26609(1994).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVB/N; TISSUE=Mammary gland;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RP FUNCTION.
 RX MEDLINE=20171264; PubMed=10704386;
 RA Imondi R., Wideman C., Kaprielian Z.;
 RT "Complementary expression of transmembrane ephrins and their receptors
 RT in the mouse spinal cord: a possible role in constraining the
 RT orientation of longitudinally projecting axons.";
 RL Development 127:1397-1410(2000).
 CC -!- FUNCTION: Binds to the receptor tyrosine kinases EPHB1 and EPHA1.
 CC Binds to, and induce the collapse of, commissural axons/growth
 CC cones in vitro. May play a role in constraining the orientation of
 CC longitudinally projecting axons.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- TISSUE SPECIFICITY: Expressed on lateral floor plate cells,
 CC specifically on commissural axon segments that have passed through
 CC the floor plate. Expressed in cells of the retinal ganglion cell
 CC layer during retinal axon guidance to the optic disc.
 CC -!- DEVELOPMENTAL STAGE: Expressed in the floor plate throughout the
 CC period of commissural axon pathfinding.
 CC -!- PTM: Inducible phosphorylation of tyrosine residues in the
 CC cytoplasmic domain.
 CC -!- SIMILARITY: Belongs to the ephrin family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U07602; AAC53247.1; -.

DR EMBL; U07598; AAC53247.1; JOINED.
 DR EMBL; U07599; AAC53247.1; JOINED.
 DR EMBL; U07600; AAC53247.1; JOINED.
 DR EMBL; Z48781; CAA88695.1; -.
 DR EMBL; U12983; AAA53231.1; -.
 DR EMBL; BC006797; AAH06797.1; -.
 DR PIR; I48780; I48780.
 DR MGD; MGI:102708; Efnb1.
 DR GO; GO:0045121; C:lipid raft; IDA.
 DR GO; GO:0007411; P:axon guidance; IMP.
 DR InterPro; IPR008972; Cupredoxin.
 DR InterPro; IPR001799; Ephrin.
 DR Pfam; PF00812; Ephrin; 1.
 DR PRINTS; PR01347; EPHRIN.
 DR ProDom; PD002533; Ephrin; 1.
 DR PROSITE; PS01299; EPHRIN; 1.
 KW Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;
 KW Signal; Phosphorylation.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 345 EPHRIN-B1.
 FT DOMAIN 25 236 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 237 257 POTENTIAL.
 FT DOMAIN 258 345 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 343 345 PDZ RECOGNITION MOTIF (POTENTIAL).
 FT DISULFID 64 101 BY SIMILARITY.
 FT DISULFID 89 153 BY SIMILARITY.
 FT CARBOHYD 139 139 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 90 90 S -> T (IN REF. 2).
 SQ SEQUENCE 345 AA; 37859 MW; 8C96FD3DC5CBC405 CRC64;

Query Match 24.7%; Score 604.5; DB 1; Length 345;
 Best Local Similarity 37.9%; Pred. No. 8.7e-33;
 Matches 136; Conservative 51; Mismatches 107; Indels 65; Gaps 10;

Qy 15 ALLLLGLVGLVSGL--SLEPVYWNSANKRFQAEAGGYVLYPQIGDRLDLLCPRARPPGPHS 72
 |::| : | : | :||| |:| | :| : | :||:|:|:|:|:| |
 Db 15 AMVVLTLCLRLATPLAKNLEPVSWSSLNPKFLSGKGLVIYPKIGDKLDIICPRAEAGRP-- 72
 Qy 73 SPNYEFYKLYLVGGAQGRRCCEAPPAPNLLTCDRDLRLFTIKFQEYSPNLWGHEFRSH 132
 ||:||||| | | ||:|:|:|:| :|||:|:|:|:| | ||: :
 Db 73 ---YEYYKLYLVRPEQAAACSTVLDPNVLVTCNKPHEIRFTIKFQEFSPNYMGLEFKKY 129
 Qy 133 HDYYIIATSDGTREGLESQGQVCLTRGMKVLLRVGQSPRGAVPRKPVSEMPMERDRGA 192
 |||| :||:|: |||: :||| || ||:|:|:| | | : : | :
 Db 130 HDYYITSTSNGLSLEGLNREGGVCRTMTKIVMKVGQDP-NAVTPEQLTTSRPSKESDNT 188
 Qy 193 AHSLEPGKENLPGDPTSNAISRGAEGP-----LPPPSMPAVAGAAGG-----LA 236
 : : | ||:| | | | |
 Db 189 VKT-----ATQAPGRGSQGDSDGKHETVNQEEKSGPGAGGGGSGDSDSFFNSK 236
 Qy 237 LLLLG VAGAGGA-----MCWRRRRRAKPSESRHPGPGSFGGGS LGL----GG 279
 : | || : |:| | : | :| |
 Db 237 VALFAAVGAGCVIFLLIIIFLTVLLKLRKRHRKHTQQ-----RAAALSSTLASP 287
 Qy 280 GGGMGPREAEPGELGIALRGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPNIIY 338
 || | || :| || : :|||:|:|:|:|:|:|:|:|:|:|:|:|
 Db 288 KGGSGTAGTEPSDIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPQSPANIY 343

RESULT 9

EFB1_RAT

ID EFB1_RAT STANDARD; PRT; 345 AA.
AC P52796;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ephrin-B1 precursor (EPH-related receptor tyrosine kinase ligand 2)
DE (LERK-2) (ELK ligand) (ELK-L).
GN EFNBI OR EPLG2 OR LERK2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95022634; PubMed=7936648;
RA Fletcher F.A., Carpenter M., Shilling H., Baum P., Ziegler S.,
RA Gimpel S., Hollingsworth T., Vanden Bos T., Davison B.L.,
RA Lyman S.D., Beckmann M.P.;
RT "LERK-2, a binding protein for the receptor-tyrosine kinase ELK, is
RT evolutionarily conserved and expressed in a developmentally regulated
RT pattern.";
RL Oncogene 9:3241-3248(1994).
CC -!- FUNCTION: Binds to the receptor tyrosine kinases EPHB3
CC (preferred), EPHB1 and EPHA1. Binds to, and induce the collapse
CC of, commissural axons/growth cones in vitro. May play a role in
CC constraining the orientation of longitudinally projecting axons
CC (By similarity).
CC -!- SUBUNIT: Binds to the receptor tyrosine kinases EPHB3 (preferred),
CC EPHB1 and EPHB2.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- PTM: Inducible phosphorylation of tyrosine residues in the
CC cytoplasmic domain (By similarity).
CC -!- SIMILARITY: Belongs to the ephrin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U07560; AAA53092.1; -.
DR PIR; I58406; I58406.
DR InterPro; IPR008972; Cupredoxin.
DR InterPro; IPR001799; Ephrin.
DR Pfam; PF00812; Ephrin; 1.
DR PRINTS; PR01347; EPHRIN.
DR ProDom; PD002533; Ephrin; 1.
DR PROSITE; PS01299; EPHRIN; 1.
KW Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;
KW Signal; Phosphorylation.

FT	SIGNAL	1	24	POTENTIAL.
FT	CHAIN	25	345	EPHRIN-B1.
FT	DOMAIN	25	236	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	237	257	POTENTIAL.
FT	DOMAIN	258	345	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	343	345	PDZ RECOGNITION MOTIF (POTENTIAL).
FT	DISULFID	64	101	BY SIMILARITY.
FT	DISULFID	89	153	BY SIMILARITY.
FT	CARBOHYD	139	139	N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ	SEQUENCE	345 AA;	37951 MW;	1B3045C5C7358F7E CRC64;

Query Match 24.5%; Score 599.5; DB 1; Length 345;
 Best Local Similarity 37.6%; Pred. No. 1.9e-32;
 Matches 135; Conservative 52; Mismatches 107; Indels 65; Gaps 10;

Qy	15	ALLLLGVLGLVSGL--SLEPVYWNSANKRFQAEGGYVLYPQIGDRDLLCPRARPPGPHS	72
Db	15	AMVVLTLCLATPLAKNLEPVSWSSSLNPKFLSGKGLVIYPKIGDKLDIICPRAEAGRP--	72
Qy	73	SPNYEFYKLYLVGGAQGRCEAPPAPNLLLTCDRDLRLFTIKFQEYSPNLWGHEFRSH	132
Db	73	---YEYYKLYLVRPEQAAACSTVLDPNVLVTCKNPQQEIRFTIKFQEFSPNYMGLEFKKY	129
Qy	133	HDYYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGA VPRKPVSEMPMERDRGA	192
Db	130	HDYYITSTSNGLSLEGLNREGGVCRTRTMKIVMKVGQDP-NAVTFEQLTTSRPSKESDNT	188
Qy	193	AHSLEPGKENLPGDPTS NATSRGAEGP-----LPPPSMPAVAGAAGG-----LA	236
Db	189	VKT-----ATQAPGRGSQGDSDGKHETVNQQEKSGPGAGGSGSGDTSFFNSK	236
Qy	237	LLLLGVAGAGGA-----MCWRRRRRAKPSES RHPGPGSFGRGGS LGL---GG	279
Db	237	VALFAAVGAGCVIFLLIIIFLTVLLKLRKRHRKHTQQ-----RAAALS LSTLASP	287
Qy	280	GGGMGPRAEPGELGIALRGGGAADPPFCPHYEKVSGDYGHPVYIVQDGPPQSPPNIIYY	338
Db	288	KDGS GTAGTEPSDIIIPLR---TTENNYCPHYEKVSGDYGHPVYIVQEMPPQSPANIIYY	343

RESULT 10

EFB1_XENLA

ID EFB1_XENLA STANDARD; PRT; 327 AA.

AC O13097;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Ephrin-B1 precursor (EPH-related receptor tyrosine kinase ligand 2)
 (LERK-2) (ELK ligand) (ELK-L) (XLERK).

GN EFNBI OR EPLG2 OR LERK2.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;

OC Xenopodinae; Xenopus.

OX NCBI_TaxID=8355;

RN [1]

RP SEQUENCE FROM N.A.

```

RX  MEDLINE=97316777; PubMed=9174051;
RA  Jones T.L., Karavanova I., Chong L., Zhou R.P., Daar I.O.;
RT  "Identification of XLerk, an Eph family ligand regulated during
RT  mesoderm induction and neurogenesis in Xenopus laevis.";
RL  Oncogene 14:2159-2166(1997).
CC  -!- FUNCTION: May have a role in the developing mesenchymal and
CC      nervous tissue.
CC  -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC  -!- TISSUE SPECIFICITY: In the adult, expressed at low levels in most
CC      adult tissues with increased levels observed in the kidney,
CC      oocytes, ovary and testis.
CC  -!- PTM: Inducible phosphorylation of tyrosine residues in the
CC      cytoplasmic domain (By similarity).
CC  -!- SIMILARITY: Belongs to the ephrin family.
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL; U31427; AAC35995.1; -.
DR  InterPro; IPR008972; Cupredoxin.
DR  InterPro; IPR001799; Ephrin.
DR  Pfam; PF00812; Ephrin; 1.
DR  PRINTS; PR01347; EPHRIN.
DR  ProDom; PD002533; Ephrin; 1.
DR  PROSITE; PS01299; EPHRIN; 1.
KW  Developmental protein; Neurogenesis; Transmembrane; Glycoprotein;
KW  Signal; Phosphorylation.
FT  SIGNAL      1      20      POTENTIAL.
FT  CHAIN       21     327     EPHRIN-B1.
FT  DOMAIN      21     225     EXTRACELLULAR (POTENTIAL).
FT  TRANSMEM    226     246     POTENTIAL.
FT  DOMAIN      247     327     CYTOPLASMIC (POTENTIAL).
FT  DOMAIN      325     327     PDZ RECOGNITION MOTIF (POTENTIAL).
FT  DISULFID    57      93      BY SIMILARITY.
FT  DISULFID    81     145      BY SIMILARITY.
FT  CARBOHYD    131     131      N-LINKED (GLCNAC. . .) (POTENTIAL).
FT  CARBOHYD    202     202      N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ  SEQUENCE    327 AA;  36621 MW;  71230CE7F6BE5974 CRC64;

Query Match      24.1%; Score 591; DB 1; Length 327;
Best Local Similarity 39.5%; Pred. No. 6.3e-32;
Matches 144; Conservative 43; Mismatches 100; Indels 78; Gaps 12;

QY      10 GVR--VGALLLLGVLGLVSGLSLEPVYWSANKRFQAEAGGYVLYPQIGDRDLDCPPRA-- 65
      |:|  :| ||:| |  | :||| ||| | | : | ||||:|||||:|:|:
Db       3 GLRRLGLLLVLYRLCSALGKNLEPVTWNSQNPRFISGKGLVLYPEIGDRLDIICPKGLF 62

QY      66 RPPGPHSSPNYEFYKLYLVGGAQGRRC EAPPAPNLLLTCDRPDLDLRFTIKFQEYSPNLW 125
      :|  ||:||||:| |  | ||:|:|:| | : |||||:|:|:|
Db       63 QP-----YEYYKLYMVRRDQLEACSTVIDPNVLVTCNQPGKEYRFTIKFQEFSPNYM 114

QY      126 GHEFRSHHDYIIATSDGTREGLES LQGGVCLTRGMKVLLRVGQSPRGGAVPRKPVSEMP 185

```


CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).

DR EMBL; Y09668; CAA70863.1; -.
 DR ZFIN; ZDB-GENE-990415-66; efna2.
 DR InterPro; IPR008972; Cupredoxin.
 DR InterPro; IPR001799; Ephrin.
 DR Pfam; PF00812; Ephrin; 1.
 DR PRINTS; PR01347; EPHRIN.
 DR ProDom; PD002533; Ephrin; 1.
 DR PROSITE; PS01299; EPHRIN; 1.
 KW Developmental protein; Neurogenesis; Glycoprotein; Lipoprotein;
 KW Membrane; GPI-anchor; Signal.
 FT SIGNAL 1 16 POTENTIAL.
 FT CHAIN 17 174 EPHRIN-A2.
 FT PROPEP 175 195 REMOVED IN MATURE FORM (POTENTIAL).
 FT DISULFID 57 97 BY SIMILARITY.
 FT LIPID 174 174 GPI-anchor amidated cysteine (Potential).
 FT CARBOHYD 32 32 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 195 AA; 22688 MW; 9EE284FEB61D0C42 CRC64;

Query Match 7.6%; Score 185; DB 1; Length 195;
 Best Local Similarity 29.9%; Pred. No. 1.4e-05;
 Matches 63; Conservative 21; Mismatches 71; Indels 56; Gaps 7;

Qy 33 VYWNSANKRFQAEAGGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGAQGRRC 92
 |||||:| || :| | : | | ||: || | || | | :| |
 Db 29 VYWSSNSRFEW-QGEYTVAVSINDYLDVYCPYYESPQPHS--RMERYILFMVNHGDLTC 85
 Qy 93 EAPPAPNLLLTCDR---PDLDLRFITKFEYSPNLWGHEFRSHHDYIIATSDGTREGLE 149
 | :| | |||: ||| :| | || | :| | | :| |
 Db 86 EHRMRGFKRWEENRQSPDGPLRFSEKFLQFTFSLGFEFRPGHEYYYISSPHPNHAGKP 145
 Qy 150 SLQGGVCLTRGMKVLRLRVGQSPRGGAVPRKPVSEMPMERDRGAHSLPEPKENLPGDPTS 209
 | : :|| : || | | | :| | |
 Db 146 CLK-----LKVYV-----KPTSS-----GYESPEPFLTD 169
 Qy 210 NATSRGAEGPLPPPSMPAVAGAAGGLALLLL 240
 : ||:| | | :| :|
 Db 170 QSQRCGADGPC-----LAVLML 186

RESULT 12

EFA3_HUMAN

ID EFA3_HUMAN STANDARD; PRT; 238 AA.
 AC P52797;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Ephrin-A3 precursor (EPH-related receptor tyrosine kinase ligand 3)
 DE (LERK-3) (EHK1 ligand) (EHK1-L).
 GN EFNA3 OR EPLG3 OR LERK3 OR EFL2.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95140419; PubMed=7838529;
 RA Kozlosky C.J., Maraskovsky E., McGrew J.T., Vanden Bos T.,
 RA Teepe M., Lyman S.D., Srinivasan S., Fletcher F.A., Gayle R.B. III,
 RA Cerretti D.P., Beckmann M.P.;
 RT "Ligands for the receptor tyrosine kinases hek and elk: isolation of
 RT cDNAs encoding a family of proteins.";
 RL Oncogene 10:299-306(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95063919; PubMed=7973638;
 RA Davis S., Gale N.W., Aldrich T.H., Maisonpierre P.C., Lhotak V.,
 RA Pawson T., Goldfarb M., Yancopoulos G.D.;
 RT "Ligands for EPH-related receptor tyrosine kinases that require
 RT membrane attachment or clustering for activity.";
 RL Science 266:816-819(1994).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Duodenum;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnierch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -!- TISSUE SPECIFICITY: Expressed in brain, skeletal muscle, spleen,
 CC thymus, prostate, testis, ovary, small intestine, and peripheral
 CC blood leukocytes.
 CC -!- SIMILARITY: Belongs to the ephrin family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>)

CC or send an email to license@isb-sib.ch).

CC -----

DR EMBL; U14187; AAC50078.1; -.

DR EMBL; L37360; AAA52368.1; -.

DR EMBL; BC017722; AAH17722.1; -.

DR PIR; I38849; I38849.

DR Genew; HGNC:3223; EFNA3.

DR MIM; 601381; -.

DR GO; GO:0005887; C:integral to plasma membrane; TAS.

DR GO; GO:0005005; F:transmembrane-ephrin receptor activity; TAS.

DR GO; GO:0007267; P:cell-cell signaling; TAS.

DR InterPro; IPR008972; Cupredoxin.

DR InterPro; IPR001799; Ephrin.

DR Pfam; PF00812; Ephrin; 1.

DR PRINTS; PR01347; EPHRIN.

DR ProDom; PD002533; Ephrin; 1.

DR PROSITE; PS01299; EPHRIN; 1.

KW Glycoprotein; Lipoprotein; Membrane; GPI-anchor; Signal.

FT SIGNAL 1 22 POTENTIAL.

FT CHAIN 23 214 EPHRIN-A3.

FT PROPEP 215 238 REMOVED IN MATURE FORM (POTENTIAL).

FT DISULFID 63 110 BY SIMILARITY.

FT LIPID 214 214 GPI-anchor amidated glycine (Potential).

FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 67 67 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CONFLICT 71 74 MISSING (IN REF. 2).

SQ SEQUENCE 238 AA; 26350 MW; 8EFD6AE8FE33FDDA CRC64;

Query Match 7.3%; Score 179; DB 1; Length 238;

Best Local Similarity 28.4%; Pred. No. 4.2e-05;

Matches 65; Conservative 24; Mismatches 80; Indels 60; Gaps 12;

Qy 7 GPGGVVRVGALLLLGLVGLVSGLSLEPVYWNSSANKRFQAEGGYVLYPQIGDRLDLLCP--R 64

Db 24 GPG-----GALG-----NRHAVYWNSSNQHLRRE-GYTVQVNVNDYLDIYCPHYN 67

Qy 65 ARPPGPHSSP---NYEFYKLYLVGGAQGRRCCEAPPAPNLLLTCDRPDL---DLRFTIKF 117

Db 68 SSGVGPGAGPGPGGGAEQYVLYMVSRRNGYRTCNASQGFK-RWECNRPHAPHSPKIFSEKF 126

Qy 118 QEYSPNLWGHEFRSHHDYIIATSDGTREGLESQGGVCLTRGMKVLLRVGQSPRGGAVP 177

Db 127 QRYSAFSLGYEFHAGHEYYYISTPTHNLH-----WKCLR--MKVFVCCASTSHSG--- 174

Qy 178 RKPVSEMP-----MERDRGAAHSLE-----PGKENLP 204

Db 175 EKPVP TLPQFTMGPNVKINVLEDFEGENPQVPKLEKSISGTSPKREHLP 223

RESULT 13

EFA2_MOUSE

ID EFA2_MOUSE STANDARD; PRT; 209 AA.

AC P52801;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Ephrin-A2 precursor (EPH-related receptor tyrosine kinase ligand 6)
DE (LERK-6) (ELF-1) (CEK7-ligand) (CEK7-L).
GN EFNA2 OR EPLG6 OR LERK6 OR ELF1 OR EPL6.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Swiss Webster; TISSUE=Brain;
RX MEDLINE=95007776; PubMed=7522971;
RA Cheng H.J., Flanagan J.G.;
RT "Identification and cloning of ELF-1, a developmentally expressed
RT ligand for the Mek4 and Sek receptor tyrosine kinases.";
RL Cell 79:157-168(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=95181289; PubMed=7876076;
RA Shao H., Lou L., Pandey A., Verderame M.F., Siever D.A., Dixit V.M.;
RT "cDNA cloning and characterization of a Cek7 receptor
RT protein-tyrosine kinase ligand that is identical to the ligand
RT (ELF-1) for the Mek-4 and Sek receptor protein-tyrosine kinases.";
RL J. Biol. Chem. 270:3467-3470(1995).
CC -!- SUBUNIT: Binds to the receptor tyrosine kinases EPHA3, EPHA4 and
CC EPHA5.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
CC (Potential).
CC -!- SIMILARITY: Belongs to the ephrin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U14941; AAA53636.1; -.
DR EMBL; U14752; AAA68520.1; -.
DR PIR; A54984; A54984.
DR MGD; MGI:102707; Efna2.
DR InterPro; IPR008972; Cupredoxin.
DR InterPro; IPR001799; Ephrin.
DR Pfam; PF00812; Ephrin; 1.
DR PRINTS; PR01347; EPHRIN.
DR ProDom; PD002533; Ephrin; 1.
DR PROSITE; PS01299; EPHRIN; 1.
KW Glycoprotein; Lipoprotein; Membrane; GPI-anchor; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 184 EPHRIN-A2.
FT PROPEP 185 209 REMOVED IN MATURE FORM (POTENTIAL).
FT DISULFID 69 110 BY SIMILARITY.
FT LIPID 184 184 GPI-anchor amidated asparagine
FT (Potential).
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 170 170 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 184 184 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 209 AA; 23586 MW; F1997545F25B9ABC CRC64;

Query Match 7.2%; Score 176; DB 1; Length 209;
Best Local Similarity 29.3%; Pred. No. 5.7e-05;
Matches 58; Conservative 19; Mismatches 69; Indels 52; Gaps 7;

Qy 33 VYWNSANKRFQAE-----GGYVLYPQIGDRLDLLCPRARPPGPHSSPNYEFYKLYLVGGA 87
| | | | : | | | | | | : | | | | : | | | | |
Db 35 VYWNRSNPRFQVSAVGDDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMERYILYMVNGE 93

Qy 88 QGRRCEAPPAPNLLLTCDRPLD---DLRFTIKFQEYSPNLWGHEFRSHHDYIIATSDGT 144
| : | : | | | : | | | | : | : | : | :
Db 94 GHASCDHRQRGFKRWE CNRPAAPGGPLKFSEKFQLFTPFSLGFEFRPGHEYYYISATP-- 151

Qy 145 REGLES LQGGVCLTRGMKVLLRVGQSPRGGA VPRKPVSEMPMERDRGAAHSLEPGKENLP 204
: | | : | | : | | | | | | | | | |
Db 152 ----PNLVDRPCLR--LKVYVR-----PTNETLY 174

Qy 205 GDP-----TSNATSRGAEG 218
| | | : | | |
Db 175 EAPEPIFTSNSSCSGLGG 192

RESULT 14

EFA2_HUMAN

ID EFA2_HUMAN STANDARD; PRT; 213 AA.
AC O43921; O76020;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Ephrin-A2 precursor (EPH-related receptor tyrosine kinase ligand 6)
DE (LERK-6) (HEK7-ligand) (HEK7-L).
GN EFNA2 OR EPLG6 OR LERK6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98126446; PubMed=9465306;
RA Cerretti D.P., Nelson N.;
RT "Characterization of the genes for mouse LERK-3/Ephrin-A3 (Epl3),
RT mouse LERK-4/Ephrin-A4 (Epl4), and human LERK-6/Ephrin-A2 (EPLG6):
RT conservation of intron/exon structure."
RL Genomics 47:131-135(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Lamerdin J.E., McCready P.M., Skowronski E., Adamson A.W.,
RA Burkhardt-Schultz K., Gordon L., Kyle A., Ramirez M., Stilwagen S.,
RA Phan H., Velasco N., Garnes J., Danganan L., Poundstone P.,
RA Christensen M., Georgescu A., Avila J., Liu S., Attix C., Andreise T.,
RA Trankheim M., Amico-Keller G., Coefield J., Duarte S., Lucas S.,
RA Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A.,
RA Montgomery M., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.O.,
RA Carrano A.V.;
RL Submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.

RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=99045414; PubMed=9826538;
 RA Aasheim H.C., Pedoutour F., Grosgeorge J., Logtenberg T.;
 RT "Cloning, chromosomal mapping, and tissue expression of the gene
 RT encoding the human Eph-family kinase ligand ephrin-A2.";
 RL Biochem. Biophys. Res. Commun. 252:378-382(1998).
 CC -!- SUBUNIT: Binds to the receptor tyrosine kinases EPHA3, EPHA4 and
 CC EPHA5.
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
 CC (Potential).
 CC -!- SIMILARITY: Belongs to the ephrin family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U92896; AAC39577.1; -.
 DR EMBL; U92893; AAC39577.1; JOINED.
 DR EMBL; U92894; AAC39577.1; JOINED.
 DR EMBL; AC004258; AAC04896.1; -.
 DR EMBL; AJ007292; CAA07435.1; -.
 DR PIR; JE0322; JE0322.
 DR Genew; HGNC:3222; EFNA2.
 DR MIM; 602756; -.
 DR GO; GO:0005106; F:ephrin; TAS.
 DR GO; GO:0007267; P:cell-cell signaling; TAS.
 DR InterPro; IPR008972; Cupredoxin.
 DR InterPro; IPR001799; Ephrin.
 DR Pfam; PF00812; Ephrin; 1.
 DR PRINTS; PR01347; EPHRIN.
 DR ProDom; PD002533; Ephrin; 1.
 DR PROSITE; PS01299; EPHRIN; 1.
 KW Glycoprotein; Lipoprotein; Membrane; GPI-anchor; Signal.
 FT SIGNAL 1 24 POTENTIAL.
 FT CHAIN 25 188 EPHRIN-A2.
 FT PROPEP 189 213 REMOVED IN MATURE FORM (POTENTIAL).
 FT DISULFID 73 114 BY SIMILARITY.
 FT LIPID 188 188 GPI-anchor amidated asparagine
 FT (Potential).
 FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 188 188 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 6 6 R -> A (IN REF. 3).
 FT CONFLICT 25 26 RA -> PP (IN REF. 3).
 FT CONFLICT 29 30 AA -> RR (IN REF. 3).
 SQ SEQUENCE 213 AA; 23878 MW; 33C9FB1A8168B2D0 CRC64;

Query Match 7.2%; Score 175.5; DB 1; Length 213;
 Best Local Similarity 36.8%; Pred. No. 6.3e-05;
 Matches 43; Conservative 14; Mismatches 51; Indels 9; Gaps 3;

QY 33 VYWNSANKRFQA-----EGGYVLYPQIGDRDLLCPRARPPGPHSSPNYEFYKLYLVGGA 87
 |||| :| || | ||| : | ||| : | | : | | ||| :| |
 Db 39 VYWNRSNPRFHAGAGDDGGGYTVEVSINDYLDIYCPHYGAPLP-PAERMEHYVLYMVNGE 97
 QY 88 QGRRCEAPPAPNLLLTCDRDL---DLRFTIKFQEYSPNLWGHEFRSHHDYIIATS 141
 |: ||| ||| :|| | ||| :||| :| :
 Db 98 GHASCDHRQRGFKRWEENRPAAPGGPLKFSEKFQLFPSLGFEPGHEYYYISAT 154

RESULT 15

EFA2_CHICK

ID EFA2_CHICK STANDARD; PRT; 200 AA.
 AC P52802;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Ephrin-A2 precursor (EPH-related receptor tyrosine kinase ligand 6)
 DE (LERK-6) (ELF-1).
 GN EFNA2 OR EPLG6 OR LERK6 OR ELF1.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95360981; PubMed=7634327;
 RA Cheng H.J., Nakamoto M., Bergemann A.D., Flanagan J.G.;
 RT "Complementary gradients in expression and binding of ELF-1 and Mek4
 RT in development of the topographic retinotectal projection map.";
 RL Cell 82:371-381(1995).
 CC -!- SUBUNIT: Binds to the receptor tyrosine kinases EPHA3, EPHA4 and
 CC EPHA5 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor
 CC (Potential).
 CC -!- TISSUE SPECIFICITY: Expressed in a gradient across the tectum
 CC being more strongly expressed at the posterior pole.
 CC -!- SIMILARITY: Belongs to the ephrin family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; L40932; AAC42229.1; -.
 DR InterPro; IPR008972; Cupredoxin.
 DR InterPro; IPR001799; Ephrin.
 DR Pfam; PF00812; Ephrin; 1.
 DR PRINTS; PR01347; EPHRIN.
 DR ProDom; PD002533; Ephrin; 1.
 DR PROSITE; PS01299; EPHRIN; 1.
 KW Glycoprotein; Lipoprotein; Membrane; GPI-anchor; Signal.
 FT SIGNAL 1 22 POTENTIAL.
 FT CHAIN 23 175 EPHRIN-A2.

